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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:45:34 ; Search time 13266.4 Seconds
(without alignments)
11198.460 Million cell updates/sec

Title: US-09-719-485-1
Perfect score: 3066
Sequence: 1 ttgaattatctgtgtaactg.....acgtgaagacgatgggataa 3066

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_to.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3066	100.0	3066	6	BD211242 Cloning a
2	3050.8	99.5	163284	9	AL137000 Human DNA
3	3050.8	99.5	341560	2	AL596304 Homo sapi
4	3050.8	99.5	349980	6	AX711879 Sequence
5	3050.8	99.5	349980	6	AX739961 Sequence
6	2026	66.1	2040	9	AF034632 Homo sapi
7	1038	33.9	1161	6	AX154591 Sequence
8	1038	33.9	1390	6	BD211244 Cloning a
9	901	29.4	1239	6	BD211243 Cloning a
10	901	29.4	1239	6	CQ724376 Sequence
11	901	29.4	1239	6	CQ831648 Sequence
12	901	29.4	1239	6	AX154589 Sequence
13	901	29.4	1239	6	AX549187 Sequence
14	901	29.4	1239	6	AX572965 Sequence
15	901	29.4	1239	9	AV603964 Homo sapi
16	900	29.4	900	6	BD211249 Cloning a
17	611.2	19.9	692	9	HS333407 Homo sapi
18	591.2	19.3	692	9	HS342408 Homo sapi
19	576.4	18.8	615	9	HS339459 Homo sapi

C 20	550.6	18.0	674	9	HSA330081	AJ330081	Homo sapi
C 21	487.8	15.9	703	9	HSA340216	AJ340216	Homo sapi
C 22	480.4	15.7	742	9	HSA340035	AJ340035	Homo sapi
C 23	478.6	15.6	807	9	HSA337736	AJ337736	Homo sapi
C 24	444.8	14.5	746	9	HSA341117	AJ341117	Homo sapi
C 25	443.8	14.5	701	9	HSA326768	AJ326768	Homo sapi
C 26	414.4	13.5	749	9	HSA323055	AJ323055	Homo sapi
C 27	411	13.4	693	9	HSA340953	AJ340953	Homo sapi
C 28	404.4	13.2	722	9	HSA340215	AJ340215	Homo sapi
C 29	402	13.1	681	9	HSA341310	AJ341310	Homo sapi
C 30	386	12.6	816	9	HSA340651	AJ340651	Homo sapi
C 31	338	11.0	602	6	BD211251	BD211251	Cloning a
C 32	307	10.0	191949	2	AC109158	AC109158	Mus muscu
C 33	285.8	9.3	573	9	HSA341295	AJ341295	Homo sapi
C 34	283	9.2	283	6	AR168467	AR168467	Sequence
C 35	283	9.2	283	6	AR182284	AR182284	Sequence
C 36	283	9.2	283	6	AR303910	AR303910	Sequence
C 37	283	9.2	283	6	BD056681	BD056681	Galanin r
C 38	283	9.2	283	6	BD064652	BD064652	Human gal
C 39	283	9.2	283	6	BD064664	BD064664	Mouse gal
C 40	250.2	8.2	1351	5	AB095997	AB095997	Gallus ga
C 41	250.2	8.2	1703	5	AB095996	AB095996	Gallus ga
C 42	250.2	8.2	1751	5	AB095995	AB095995	Gallus ga
C 43	250.2	8.2	4121	5	AB095994	AB095994	Gallus ga
C 44	248.2	8.1	1050	6	BD222611	BD222611	Canine gr
C 45	248.2	8.1	1050	6	AR429668	AR429668	Sequence

ALIGNMENTS

RESULT 1
BD211242
LOCUS BD211242 3066 bp DNA linear PAT 17-JUL-2003
DEFINITION Cloning and identification of motilin receptor.
ACCESSION BD211242
VERSION BD211242.1 GI:33021012
KEYWORDS JP 2002517507-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3066)
AUTHORS Feighner,S.D., Patchett,A.A., Tan,C., Mckee,K., Macnei,D.,
Howard,A.D., Pong,S.S. and Smith,R.G.
TITLE Cloning and identification of motilin receptor
JOURNAL Patent: JP 2002517507-A 1 18-JUN-2002;
COMMENT MERCK AND CO INC
OS Homo sapiens (human)
PN JP 2002517507-A/1
PD 18-JUN-2002
PF 08-JUN-1999 JP 2000553444
PR 12-JUN-1998 US 60/089098
PI SCOTT D FEIGNER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI
DOUGLAS MACNEIL,
PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH
PC C07K14/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02, PC
C12N15/00
CC Cloning and identification of motilin receptor. FH Key
FT source
FT Location/Qualifiers
1..3066
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES

Query Match 100.0%; Score 3066; DB 6; Length 3066;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3066; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAAATTATCTGGTCACTGCGGCGCGGTGGGTGAGTCAAGCCTGTAAATCCAGCACTTTGG 60
DB 1 TTGAAATTATCTGGTCACTGCGGCGCGGTGGGTGAGTCAAGCCTGTAAATCCAGCACTTTGG 60
QY 61 GAGTTCGAGCGGGTGGACCACTTGGGTGAGGAGTTCGAGACACAGGCTGGCCAAACATGG 120
DB 61 GAGTTCGAGCGGGTGGACCACTTGGGTGAGGAGTTCGAGACACAGGCTGGCCAAACATGG 120
QY 121 CGAAACCTCTGACTACACAAAAACA CA AAAATTTAGCGGGGCTTGGGCGCTCTGTGCTC 180
DB 121 CGAAACCTCTGACTACACAAAAACA CA AAAATTTAGCGGGGCTTGGGCGCTCTGTGCTC 180
QY 181 CCAGTCTACTCAGGAGGCTGAGTGGAGGACCTGCTTGGAGCTGGAGGCTGAGGCTGAG 240
DB 181 CCAGTCTACTCAGGAGGCTGAGTGGAGGACCTGCTTGGAGCTGGAGGCTGAGGCTGAG 240
QY 241 TCAGTCTGTGATCGCGCACTTAAACTCCAGCCTGGACGACAGTGGAGCCCTGTCTCAAGA 300
DB 241 TCAGTCTGTGATCGCGCACTTAAACTCCAGCCTGGACGACAGTGGAGCCCTGTCTCAAGA 300
QY 301 AGAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 360
DB 301 AGAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 360
QY 361 GGTACGCTCCCTCCACCACTCGGAACTTACAGAGAGGAGAACTGGGCTGGGCGAGACC 420
DB 361 GGTACGCTCCCTCCACCACTCGGAACTTACAGAGAGGAGAACTGGGCTGGGCGAGACC 420
QY 421 AGGACTAGCCCAAGATTACACAAGTTACTCGGTGTGTAGAGCCAGGATTAGACAGAGAGG 480
DB 421 AGGACTAGCCCAAGATTACACAAGTTACTCGGTGTGTAGAGCCAGGATTAGACAGAGAGG 480
QY 481 CTCTAGATTCTGTCTAGACTCCCTCTCTATTTATTTAGCAATTTATGGTCTCTGAGGATTA 540
DB 481 CTCTAGATTCTGTCTAGACTCCCTCTCTATTTATTTAGCAATTTATGGTCTCTGAGGATTA 540
QY 541 CCATGAGCCCTCTCCACCGTCAAGCGGAGCTTACCAGCCACAGACAGATCCCTTCCA 600
DB 541 CCATGAGCCCTCTCTCCACCGTCAAGCGGAGCTTACCAGCCACAGACAGATCCCTTCCA 600
QY 601 AGGTGCGCGGAGTACAGACTGACAAAGCGCCGTACAGTGTCTAGTCTGTGTAACCAAA 660
DB 601 AGGTGCGCGGAGTACAGACTGACAAAGCGCCGTACAGTGTCTAGTCTGTGTAACCAAA 660
QY 661 GCTGTCTAGGCTGAGACTGCTCACCGGACCGGTGAGGCTGCTGAGGCGGC 720
DB 661 GCTGTCTAGGCTGAGACTGCTCACCGGACCGGTGAGGCTGCTGAGGCGGC 720
QY 721 GGGTATTTCCAGTTAGTGGAGGGAAGCGCCCTGGAACTGSCATGGGCCCCGGGAGAGGGCG 780
DB 721 GGGTATTTCCAGTTAGTGGAGGGAAGCGCCCTGGAACTGSCATGGGCCCCGGGAGAGGGCG 780
QY 781 CGGAGCGGAGCATGCGCGGCGCGGCGCGGCGCGGCGCGTGGGCGGAGACTGCGGCGAG 840
DB 781 CGGAGCGGAGCATGCGCGGCGCGGCGCGGCGCGGCGCGTGGGCGGAGACTGCGGCGAG 840
QY 841 CTAGCTCGGAGCGCTCGAGCCACCCGCGAGCGCGTCTCGCGCGCCCCCGAGCGCA 900
DB 841 CTAGCTCGGAGCGCTCGAGCCACCCGCGAGCGCGTCTCGCGCGCCCCCGAGCGCA 900
QY 901 CGCGAGCGCTCGCGCGCTGACCTGCGCGCGCGCGCGCGTGGGCTGGGAAAGAGGGCG 960
DB 901 CGCGAGCGCTCGCGCGCTGACCTGCGCGCGCGCGCGCGTGGGCTGGGAAAGAGGGCG 960
QY 961 CTCACGAGAGGACACCGCGCGAGTCCAGCCCGAGCCCGGAGCGCGCGCGCGCGCG 1020
DB 961 CTCACGAGAGGACACCGCGCGAGTCCAGCCCGAGCCCGGAGCGCGCGCGCGCGCG 1020
QY 1021 GAGCACCATGGGAGCCCTTGGAAAGCGGACGCGCCCGAGGCGCGCGGCGCGCGCG 1080
DB 1021 GAGCACCATGGGAGCCCTTGGAAAGCGGACGCGCCCGAGGCGCGCGGCGCGCGCG 1080
QY 1081 CGTGGCGCGCGTGGCGCTTGGGAGAGCGCGCGTGTGCGCCCTTTCCCTCGGGGGCG 1140

DB 1081 CGTGGCGCGCGTGGCGCTTGGGAGAGCGCGTGTGCGCCCTTCCCTCGGGGGCGC 1140
QY 1141 TGGTGGCGGTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 1141 TGGTGGCGGTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 TGACCGTGTATGCTGATCGGCGCTACCGGGAATGCGGACCAACCAACCACTGTGTACCTGG 1260
DB 1201 TGACCGTGTATGCTGATCGGCGCTACCGGGAATGCGGACCAACCAACCACTGTGTACCTGG 1260
QY 1261 GCAGCATGCGGTGTGCTGACCTACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1261 GCAGCATGCGGTGTGCTGACCTACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
QY 1321 TCTGGCGCTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1321 TCTGGCGCTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1381 GCGAGGCTGCACTACCGCACGCTGCTGCAATGACCGGCTCAGGCTCAGGCTGAGGCTACC 1440
DB 1381 GCGAGGCTGCACTACCGCACGCTGCTGCAATGACCGGCTCAGGCTCAGGCTGAGGCTACC 1440
QY 1441 TGGCCATCTGCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 TGGCCATCTGCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1501 TCATCGCTGTGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1501 TCATCGCTGTGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 GCGTTCGAGCAGGACCCCGGCACTCTCCGTAGTCCCGGCTCAATGGCACCGCGCGGATCG 1620
DB 1561 GCGTTCGAGCAGGACCCCGGCACTCTCCGTAGTCCCGGCTCAATGGCACCGCGCGGATCG 1620
QY 1621 CCTCTCGCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1621 CCTCTCGCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 GCGCGTTCGCGGCGCGGAGACCGCGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
DB 1681 GCGCGTTCGCGGCGCGGAGACCGCGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1741 GCGCGCGCGAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
DB 1741 GCGCGCGCGAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
QY 1801 TGCCCTTTCTGCTGCTCAGCATCTCTACGCGCTCATCGGCGGAGCTGTGGAGCAGCC 1860
DB 1801 TGCCCTTTCTGCTGCTCAGCATCTCTACGCGCTCATCGGCGGAGCTGTGGAGCAGCC 1860
QY 1861 GCGCGCGCTGCGAGGCGCGCGCTCGGCGGCGGAGAGGCGCACCGGCGAGACCGCTTC 1920
DB 1861 GCGCGCGCTGCGAGGCGCGCGCTCGGCGGCGGAGAGGCGCACCGGCGAGACCGCTTC 1920
QY 1921 GCGTCTG 1980
DB 1921 GCGTCTG 1980
QY 1981 CGGCGGACCGCGCAACAGCTGGGTCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
DB 1981 CGGCGGACCGCGCAACAGCTGGGTCCTTCCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
QY 2041 CAGCTCCCTCTTATTTGATTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCC 2100
DB 2041 CAGCTCCCTCTTATTTGATTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCC 2100
QY 2101 ACCATGCTG 2160
DB 2101 ACCATGCTG 2160
QY 2161 CGGATCCGATTCAGTTAACAGCAGTGTCTTTCCAGGCTCTGAGACCTCTGAGACCAAGAGGAGCT 2220

repeat_region	/note="AluSc repeat: matches 1. .85 of consensus"	9887. .10191	repeat_region	/note="L1M23 repeat: matches 5724. .5874 of consensus"	30814. .30947
repeat_region	/note="AluX repeat: matches 1. .306 of consensus"	12201. .12247	repeat_region	/note="MIR repeat: matches 175. .262 of consensus"	33134. .33214
repeat_region	/note="L2 repeat: matches 2704. .2750 of consensus"	12472. .12738	repeat_region	/note="MIR repeat: matches 175. .262 of consensus"	35454. .35753
repeat_region	/note="L2 repeat: matches 1304. .1530 of consensus"	12739. .12874	misc_feature	/note="AluX repeat: matches 1. .300 of consensus"	36245. .36743
repeat_region	/note="FLAM_C repeat: matches 2. .133 of consensus"	12875. .12887	repeat_region	/note="match: GSS: Em:AQ593229"	36556. .36843
repeat_region	/note="L2 repeat: matches 1530. .1542 of consensus"	12922. .13227	misc_feature	/note="MIR repeat: matches 14. .237 of consensus"	38014. .38191
repeat_region	/note="L1M23 repeat: matches 5871. .6183 of consensus"	13303. .13348	repeat_region	/note="match: STS: Em:G04228"	38279. .38416
repeat_region	/note="MLR1E repeat: matches 1. .46 of consensus"	13533. .13623	repeat_region	/note="MER5A repeat: matches 7. .152 of consensus"	39603. .39708
repeat_region	/note="MLR1E repeat: matches 223. .315 of consensus"	13657. .13865	repeat_region	/note="MIR repeat: matches 34. .144 of consensus"	40037. .40103
repeat_region	/note="MLR1E repeat: matches 307. .533 of consensus"	13890. .14150	repeat_region	/note="L2 repeat: matches 2664. .2731 of consensus"	40370. .40523
repeat_region	/note="MLR1J repeat: matches 195. .456 of consensus"	14151. .14450	repeat_region	/note="L2 repeat: matches 2562. .2701 of consensus"	40524. .40810
repeat_region	/note="AluSg repeat: matches 1. .307 of consensus"	14501. .14729	repeat_region	/note="AluX repeat: matches 2. .297 of consensus"	40811. .41080
repeat_region	/note="L1Mac repeat: matches 588. .813 of consensus"	14730. .15006	repeat_region	/note="L2 repeat: matches 2242. .2562 of consensus"	41085. .41156
repeat_region	/note="AluDo repeat: matches 1. .285 of consensus"	15007. .15361	repeat_region	/note="L2 repeat: matches 2626. .2697 of consensus"	41549. .41871
repeat_region	/note="L1Mac repeat: matches 813. .1178 of consensus"	15389. .15437	misc_feature	/note="MER2 repeat: matches 1. .343 of consensus"	complement(42041. .42676)
repeat_region	/note="L1Mac repeat: matches 1159. .1207 of consensus"	15438. .16412	repeat_region	/note="match: GSS: Em:AQ112495"	42192. .48502
repeat_region	/note="HERVL repeat: matches 2891. .3879 of consensus"	16413. .16616	repeat_region	/note="LIP7 repeat: matches 128. .6143 of consensus"	49671. .49794
repeat_region	/note="MLT2B repeat: matches 1. .216 of consensus"	17092. .17141	repeat_region	/note="L2 repeat: matches 2617. .2748 of consensus"	50285. .50483
repeat_region	/note="MER5B repeat: matches 27. .79 of consensus"	17416. .17647	repeat_region	/note="L1M23 repeat: matches 5985. .6183 of consensus"	50630. .50815
repeat_region	/note="MIR repeat: matches 17. .261 of consensus"	19402. .19499	repeat_region	/note="MIR repeat: matches 10. .203 of consensus"	50979. .51656
repeat_region	/note="HY3 repeat: matches 2. .99 of consensus"	20730. .21163	repeat_region	/note="L2 repeat: matches 855. .1521 of consensus"	51654. .51892
repeat_region	/note="L2 repeat: matches 2168. .2609 of consensus"	25800. .25825	repeat_region	/note="L2 repeat: matches 1702. .1927 of consensus"	51893. .52189
repeat_region	/note="L3 copies 2 mer tt 92% conserved"	26041. .26131	repeat_region	/note="AluSg repeat: matches 1. .297 of consensus"	52190. .52379
repeat_region	/note="FLAM_C repeat: matches 17. .107 of consensus"	26144. .26249	repeat_region	/note="L2 repeat: matches 1927. .2153 of consensus"	
repeat_region	/note="53 copies 2 mer tt 64% conserved"	27029. .27259	Query Match	99.5%; Score 3050.8; DB 9; Length 163284;	
repeat_region	/note="MIR repeat: matches 2. .251 of consensus"	27422. .27788	Best Local Similarity	99.9%; Pred. No. 0;	
repeat_region	/note="L2 repeat: matches 1879. .2259 of consensus"	27863. .28239	Matches 3064; Conservative	0; Mismatches 2; Indels 2; Gaps 1;	
repeat_region	/note="L2 repeat: matches 1278. .1734 of consensus"	28255. .28571			
repeat_region	/note="AluY repeat: matches 1. .310 of consensus"	28729. .29128	Qy 1 TTGAATTAATCTGCTCACTGCGCGCGGTGCACGCTGTAATCCAGACACTTTGG 60		
repeat_region	/note="L1M23 repeat: matches 4905. .5326 of consensus"	29170. .29413	Db 143320 TTGAATTAATCTGCTCACTGCGCGCGGTGCACGCTGTAATCCAGACACTTTGG 143379		
repeat_region	/note="L1M23 repeat: matches 5461. .5715 of consensus"	29448. .29681	Qy 61 GAGGTCGAGGCGGTGGACCACTGGGGTTCAGAGGTTTCGAGACAGAGCTGGCCAACTGG 120		
repeat_region	/note="L2 repeat: matches 1594. .1828 of consensus"	29683. .29886	Db 143380 GAGGTCGAGGCGGTGGACCACTGGGGTTCAGAGGTTTCGAGACAGAGCTGGCCAACTGG 143439		
repeat_region	/note="L1M2 repeat: matches 5527. .5734 of consensus"	29888. .30323	Qy 121 CGAAACCTGACTACACAAAAACAAAAATTTAGCCGGGCTTGGGGCTCTCTGTGCTC 180		
repeat_region	/note="L2 repeat: matches 2129. .2596 of consensus"	30324. .30620	Db 143440 CGAAACCTGACTACACAAAAACAAAAATTTAGCCGGGCTTGGGGCTCTCTGTGCTC 143499		
repeat_region	/note="Aluwb repeat: matches 1. .299 of consensus"	30621. .30780	Qy 181 CCAGCTACTCAGGAGGCTGAGGTGGAGGACTGCTTGAGCCTGGAGGTCGAGGCTCGAG 240		
repeat_region	/note="L2 repeat: matches 2596. .2749 of consensus"	30784. .30813	Db 143500 CCAGCTACTCAGGAGGCTGAGGTGGAGGACTGCTTGAGCCTGGAGGTCGAGGCTCGAG 143559		
repeat_region	/note="L3 copies 2 mer aa 86% conserved"		Qy 241 TGAGTGTGATCGGCCACTTAAACTCCAGCTCGACAGCAGTGAAGCCCTGTCTCAAGA 300		
			Db 143560 TGAGTGTGATCGGCCACTTAAACTCCAGCTCGACAGCAGTGAAGCCCTGTCTCAAGA 143619		
			Qy 301 AGAAAAAGAAAGAAAGAAAGAAAAAGAAAAAGAAATTTTGGTCAATATATAT 360		

QY	2519	CATATGGAGCCTACTATGCAAGTTTAAAGCAAGTATCCATGAGCCTGAGCCTGGTCA	2578
Db	145840	CATATGGAGCCTACTATGCAAGTTTAAAGCAAGTATCCATGAGCCTGAGCCTGGTCA	145899
QY	2579	TTTTTCTGGGTGAGGATCTGCCTAGTAGAAGTTTCTCTAATTTATTTGCTGTAC	2638
Db	145900	TTTTTCTGGGTGAGGATCTGCCTAGTAGAAGTTTCTCTAATTTATTTGCTGTAC	145959
QY	2639	TTGTTATTGACATGGTTCCTTGTCGGGTGGGGGTTTATTGCTTCCCAATCTTTTG	2698
Db	145960	TTGTTATTGACATGGTTCCTTGTCGGGTGGGGGTTTATTGCTTCCCAATCTTTTG	146019
QY	2699	TTAATCCCGGTCTGTGCTTATGTTGAGTGGTGGTCTTGGCATTTATATTGCT	2758
Db	146020	TTAATCCCGGTCTGTGCTTATGTTGAGTGGTGGTCTTGGCATTTATATTGCT	146079
QY	2759	GGTTCGCTTCCAGTTGCGCAATCTTACATAACACGGAAGATTCGGGATGATGT	2818
Db	146080	GGTTCGCTTCCAGTTGCGCAATCTTACATAACACGGAAGATTCGGGATGATGT	146139
QY	2819	ACTTCTCTCAGTACTTTAATCATCGTCTGCTCTCAACTTTCTATCTGAGCGCATCTATCA	2878
Db	146140	ACTTCTCTCAGTACTTTAATCATCGTCTGCTCTCAACTTTCTATCTGAGCGCATCTATCA	146199
QY	2879	ACCAATCTCTACACCTCATTTCAAGAAGTACAGAGCGCGCTTTAACTGTGTC	2938
Db	146200	ACCAATCTCTACACCTCATTTCAAGAAGTACAGAGCGCGCTTTAACTGTGTC	146259
QY	2939	TGCAAGGAGTCCAGCGGAGAGGCTTCCACAGAAGCAGGACACTGCGGGGAAGTTG	2998
Db	146260	TGCAAGGAGTCCAGCGGAGAGGCTTCCACAGAAGCAGGACACTGCGGGGAAGTTG	146319
QY	2999	CAGGGACACTGAGGAGACACGGTGGGCTACACGAGCAAGCGCTAACGTGAAGACA	3058
Db	146320	CAGGGACACTGAGGAGACACGGTGGGCTACACGAGCAAGCGCTAACGTGAAGACA	146379
QY	3059	TGGGATAA 3066	
Db	146380	TGGGATAA 146387	
RESULT 3			
AL596304		341560 bp DNA linear HTG 09-AUG-2001	
LOCUS		Homo sapiens chromosome 13 clone RP11-804, 3 unordered pieces.	
DEFINITION		AL596304	
ACCESSION		AL596304	
VERSION		AL596304.3 GI:15147703	
KEYWORDS		HTG; HTGS PHASE1; HTGS CANCELLED.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		Clark, G.	
JOURNAL		Direct Submission	
COMMENT		Submitted (08-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,	
		CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk	
		requests: clonerrequest@sanger.ac.uk	
		On Aug 10, 2001 this sequence version replaced gi:15131387.	
		----- Genome Center	
		Center: Sanger Centre	
		Web site: http://www.sanger.ac.uk	
		Contact: humquery@sanger.ac.uk	
		----- Project Information	
		Center project name: BA804	
		----- Summary Statistics	
		Assembly program: XGAP4; version 4.5	
		Sequencing vector: plasmid; 108752; 100% of reads	
		Chemistry: Dye-terminator Big Dye; 100% of reads	
		Consensus quality: 149716 bases at least Q40	
		Consensus quality: 150039 bases at least Q30	
		Consensus quality: 150247 bases at least Q20	

Insert size: 341360; sum-of-contigs			
Insert size: 157238; 2.0% error; agarose-fp			
Quality coverage: 3.92x in Q20 bases; sum-of-contigs Quality			
coverage: 8.77x in Q20 bases; agarose-fp			

* NOTE: This is a 'working draft' sequence. It currently			
* consists of 3 contigs. The true order of the pieces			
* is not known and their order in this sequence record is			
* arbitrary. Gaps between the contigs are represented as			
* runs of N, but the exact sizes of the gaps are unknown.			
* This record will be updated with the finished sequence			
* as soon as it is available and the accession number will			
* be preserved.			
* 1 146853: contig of 146853 bp in length			
* 146854 146953: gap of 100 bp			
* 146954 338660: contig of 191707 bp in length			
* 338661 338760: gap of 100 bp			
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VERSION AX711879.1 GI:29787684
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AUTHORS Zhang, Y., Moffatt, M., Cookson, W. and Tinsley, J.O.
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QY 2347 TAAAGTAAACCTTCTGCTGCTATCAAAAAGTAAAGATTGTGCAGACCTGTTGTAGAAATCTTT 2406
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QY 2467 CGGCTGCTTCAGAGAAATTCCTCTCTGCTGTTATGTCCAGCCTTGATAACACATATGGG 2526
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QY 2527 AGCCTACTATGCGAGTTTAAAGCAAGTATCCATGCGAGCTGCGAGCCTGCTGCTTTTCT 2586
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QY 2887 CTCTAACCTCATTTTCAAGAAATGACAGCGCGGCTTTAACTGCTCTCGCAAGG 2946
Db 1861 CTCTAACCTCATTTTCAAGAAATGACAGCGCGGCTTTAACTGCTCTCGCAAGG 1920
QY 2947 AAGTCCAGCGCGAGAGGCTTCCACAGAGCAGGAGACACTGCGGGGAAGTTGCGAGGGAC 3006
Db 1921 AAGTCCAGCGCGAGAGGCTTCCACAGAGCAGGAGACACTGCGGGGAAGTTGCGAGGGAC 1980
QY 3007 ACTGAGGAGACACGTTGGGCTACACCGAGACAAAGCGCTAAACGTAAGACATGGGATAA 3066
Db 1981 ACTGAGGAGACACGTTGGGCTACACCGAGACAAAGCGCTAAACGTAAGACATGGGATAA 2040

RESULT 7
AX154591
LOCUS AX154591 1161 bp DNA linear PAT 23-JUN-2001
DEFINITION Sequence 11 from Patent WO0138355.
ACCESSION AX154591
VERSION AX154591.1 GI:14536177
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sheppard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D.
TITLE Method of forming a peptide-receptor complex with zsig33 and
therapeutic use thereof
JOURNAL Patent: WO 0138355-A 11 31-MAY-2001;
ZymoGenetics, Inc. (US)
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ORIGIN

Query Match 33.9%; Score 1038; DB 6; Length 1161;
Best Local Similarity 99.8%; Pred. No. 8e-153;
Matches 1050; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1029 ATGGGACGCCCTGGAACGGCAGCGACCGCCCGGAGGGGGCGGAGCGCGCGTGGGCC 1088
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Qy 1089 GCGTGGCGCCTTGGCAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGCTGCGG 1148
Db 61 GCGTGGCGCCTTGGCAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGCTGCGG 120

Qy 1149 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208
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Qy 1209 ATGCTGATCGGGCGCTACCGGACATCGGACACCACTTGTACCTGTACCGCTCTGGCGC 1328
Db 241 GCGGTGTCCGACCTACTCATCTGCTGCGGCTGCGGCTTGCACCTGTACCGCTCTGGCGC 300

Qy 1329 TCGGGCGCCTGGGTGTTGGGCGCTGCTGCGCGCTTGTGCTGCTGCTGCTGCTGCTGCTG 1388
Db 301 TCGGGCGCCTGGGTGTTGGGCGCTGCTGCGCGCTTGTGCTGCTGCTGCTGCTGCTGCTG 360

Qy 1389 TGCACCTAGCCAGCAGCTCTGCACATGACCGGCTCAGCGCTGAGCGCTACTGSCCATC 1448
Db 361 TGCACCTAGCCAGCAGCTCTGCACATGACCGGCTCAGCGCTGAGCGCTACTGSCCATC 420

Qy 1449 TGCCGCCGCTCGCGCGCGCTTGTGCTACCGCGCGCGCTGCGCGCTCATCGCT 1508
Db 421 TGCCGCCGCTCGCGCGCGCTTGTGCTACCGCGCGCGCTGCGCGCTCATCGCT 480

Qy 1509 TGCTCTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1568
Db 481 TGCTCTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

Qy 1569 CAGGACCCCGCATCTCCGTAGTCCGGCGCTCAATGACCGCGCGCATCGCTCTCTCG 1628
Db 541 CAGGACCCCGCATCTCCGTAGTCCGGCGCTCAATGACCGCGCGCATCGCTCTCTCG 600

Qy 1629 CCTTCGCTCGTCCGCGCTCTTCGCTGCTGCGGGCGCCACCGCGCTCCCGCGCTCG 1688
Db 601 CCTTCGCTCGTCCGCGCTCTTCGCTGCTGCGGGCGCCACCGCGCTCCCGCGCTCG 660

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Qy 1809 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGCGCGCG 1868
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGCGCGCG 840

Qy 1869 CTGCGAGCGCGCGCTGCGGGCGGAGAGAGGCGCACCGGCGAGACCGCTCGCGTCTCTG 1928
Db 1881 ATGCTGATCGGGCGCTACCGGGGACATCGGAGACCAACCACTTGTACCTGGGCGAGCATG 240

Db 841 CTGCGAGCGCCGCGCGCTGCTGCGGGCGGAGAGAGCCACCGGACAGCGTCCGCGTCTG 900
Qy 1929 CGTAAGTGGAGCGCGCGTGGTTCCAAAGACGCCCTGCTGCACTGCGCCCGCGGGGACC 1988
Db 901 CGTAAGTGGAGCGCGCGTGGTTCCAAAGACGCCCTGCTGCACTGCGCCCGCGGGGACC 960
Qy 1989 GCGCAACAGCTGGGTGCCCTTTCCCTGCTGCCAGCTCTGCGGGCGCGCTTCCAGCTCCC 2048
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Qy 2049 --TCCTATTTCGATTCAGAGCTCCACCGCGCG 2078
Db 1021 TTTCTATTTCGATTCAGAGCTCCACCGCGCG 1052

RESULT 8
BD211244
LOCUS BD211244 1390 bp DNA linear PAT 17-JUL-2003
DEFINITION Cloning and identification of motilin receptor.
ACCESSION BD211244
VERSION BD211244.1 GI:33021014
KEYWORDS JP 2002517507-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1390)
AUTHORS Feighner,S.D., Patchett,A.A., Tan,C., Mckee,K., Macnei,D.,
Howard,A.D., Pong,S.S. and Smith,R.G.
TITLE Cloning and identification of motilin receptor
JOURNAL Patent: JP 2002517507-A 3 18-JUN-2002;
MERCK AND CO INC
COMMENT OS Homo sapiens (human)
PN JP 2002517507-A/3
PD 18-JUN-2002
PF 08-JUN-1999 JP 2000553444
PR 12-JUN-1998 US 60/089098
PI SCOTT D FEIGNER,ARTHUR A PATCHETT,CARINA TAN,KAREN MCKEE, PI
DOUGLAS MACNEIL,
PI ANDREW D HOWARD,SHENG SHUNG PONG,ROY G SMITH
PC C07K14/705,A61K38/00,A61P1/00,Cl2N15/09,Cl2Q1/02,A61K37/02, PC
Cl2N15/00
CC Cloning and identification of motilin receptor. FH Key
Location/Qualifiers
FT source 1..1390
Location/Qualifiers
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ORIGIN

Query Match 33.9%; Score 1038; DB 6; Length 1390;
Best Local Similarity 99.8%; Pred. No. 8e-153;
Matches 1050; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1029 ATGGGACGCCCTGGAACGGCAGCGACCGCCCGGAGGGGGCGGAGCGCGCGTGGGCC 1088
Db 1 ATGGGACGCCCTGGAACGGCAGCGACCGCCCGGAGGGGGCGGAGCGCGCGTGGGCC 60

Qy 1089 GCGTGGCGCCTTGGCAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGCTGCGG 1148
Db 61 GCGTGGCGCCTTGGCAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCTGCTGCGG 120

Qy 1149 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208
Db 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

Qy 1209 ATGCTGATCGGGCGCTACCGGACATCGGACACCACTTGTACCTGTACCGCTCTGGCGC 1268
Db 181 ATGCTGATCGGGCGCTACCGGGGACATCGGAGACCAACCACTTGTACCTGGGCGAGCATG 240


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QY 1749 CAGCTGGGCGCGCTCGTGTCTATGCTGGGTACACCGCCTACTTCTTCTGCGCTTT 1808
Db 721 CAGCTGGGCGCGCTCGTGTCTATGCTGGGTACACCGCCTACTTCTTCTGCGCTTT 780
QY 1809 CTGTGCTCAGCATCTCTACCGGCTCATCGGGCGGAGCTGTGAGAGCGCGGCGCG 1868
Db 781 CTGTGCTCAGCATCTCTACCGGCTCATCGGGCGGAGCTGTGAGAGCGCGGCGCG 840
QY 1869 CTGCGAGGCGCGCGCTCGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1928
Db 841 CTGCGAGGCGCGCGCTCGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 1929 C 1929
Db 901 C 901

RESULT 10
LOCUS CQ724376 1239 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 10310 from Patent WO02068579.
ACCESSION CQ724376
VERSION CQ724376.1 GI:42285233
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 10310 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
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ORIGIN
Query Match 29.4%; Score 901; DB 6; Length 1239;
Best Local Similarity 100.0%; Pred. No. 2.3e-131;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1029 ATGGGAGCCCTGGAAACGGACAGCGGCCCGGAGGGGCGCGGAGCGCGCGTGGCCC 1088
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Db 61 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGCCCTTCCCTCGGGGCGCTGTGCGG 120
QY 1149 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208
Db 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
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Db 181 ATGCTGTATGCGGCGCTACCGGAGCATGGGAGCACACCACTTGTACTGGGAGCATG 240
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QY 1509 GTGCTCTGGGCGGTGGCGCTGCTCTCTCCCGGTCCCTTCTTGTCTCTGGTGGCGTCCAG 1568
Db 481 GTGCTCTGGGCGGTGGCGCTGCTCTCTCCCGGTCCCTTCTTGTCTCTGGTGGCGTCCAG 540
QY 1569 CAGGACCCCGGCATCTCCGTAGTCCCGGCGCTCAATGACCGCGGAGTCCGCTCTCTCG 1628
Db 541 CAGGACCCCGGCATCTCCGTAGTCCCGGCGCTCAATGACCGCGGAGTCCGCTCTCTCG 600
QY 1629 CCTCTCGGCTCTGTCGCGCGCTCTCTGCGTCTCTCGGGGCGCGCACCGCGCTCCGCGCTCG 1688
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QY 1689 GGGCGCGAGACCGCGGAGCGCGCGCTGTTTACGCGCGGAATGCGGCGCGAGCGCGCG 1748
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QY 1869 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1928
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QY 1929 C 1929
Db 901 C 901

RESULT 11
LOCUS CQ831648 1239 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1 from Patent WO2004057328.
ACCESSION CQ831648
VERSION CQ831648.1 GI:50831561
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Golz,S., Bruggemeier,U. and Summer,H.
TITLE Diagnostics and therapeutics for diseases associated with
JOURNAL g-protein-coupled receptor 38 (gpr38)
Bayer HealthCare AG (DE)
FEATURES
source
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ORIGIN
Query Match 29.4%; Score 901; DB 6; Length 1239;
Best Local Similarity 100.0%; Pred. No. 2.3e-131;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1029 ATGGGAGCCCTGGAAACGGACAGCGGCCCGGAGGGGCGCGGAGCGCGCGTGGCCC 1088
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Db 61 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGCCCTTCCCTCGGGGCGCTGTGCGG 120
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Db 301 TCGCGGCGCTGCGGTGTTGCGGCGCTGTCTTCGCGCGCTGTCTCTACGTGGCGAGGCG 360
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Qy 1809 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGGAGACGCGCGCGCG 1868
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGGAGACGCGCGCGCG 840
Qy 1869 CTGCGAGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACACCGTCCGGTCTCTG 1928
Db 841 CTGCGAGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACACCGTCCGGTCTCTG 900
Qy 1929 C 1929
Db 901 C 901

RESULT 13
AX549187
LOCUS AX549187 1239 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 472 from Patent WO02061087.
ACCESSION AX549187
VERSION AX549187.1 GI:25813904
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
REFERENCE
AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 472 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
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ORIGIN
Query Match 29.4%; Score 901; DB 6; Length 1239;
Best Local Similarity 100.0%; Pred. No. 2.3e-131;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1029 ATGGCAGCCCTGTGAACCGGACGACCGGCCCGAGGGGCGCGGAGCGCGCGCGCC 1088
Db 1 ATGGCAGCCCTGTGAACCGGACGACCGGCCCGAGGGGCGCGGAGCGCGCGCGCGCC 60
Qy 1089 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGGCTTCCCTGGGGCGCTGTGCGG 1148
Db 61 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGGCTTCCCTGGGGCGCTGTGCGG 120
Qy 1149 GTGACCGCTGTGTGCTGTGCTGTGCTGCTGCGGGGTGAGCGGCAAGCTGTGACCGTG 1208
Db 121 GTGACCGCTGTGTGCTGTGCTGTGCTGCTGCGGGGTGAGCGGCAAGCTGTGACCGTG 180
Qy 1209 ATGTGTATGGCGCGCTACCGGAGCATGCGGACCAACCACTGTGTACCTGGGAGCATG 1268
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Qy 1269 GCGGTGTCGACCTACTCTGCTCGGCTGCGGCTTCCCTGTGACCTGTACCGCTTGGGCG 1328
Db 241 GCGGTGTCGACCTACTCTGCTCGGCTGCGGCTTCCCTGTGACCTGTACCGCTTGGGCG 300
Qy 1329 TCGCGGCGCTTGGGTGTGGGCGCGTGTCTGCGCGCTGTGCTGTGCGGCGCTGTGCTGT 1388
Db 301 TCGCGGCGCTTGGGTGTGGGCGCGTGTCTGCGCGCTGTGCTGTGCGGCGCTGTGCTGT 360
Qy 1389 TGCACCTACGCCACGCTGCTGCACATGACCGGCTGTGACGCTGTGACGCTACCTGGCCATC 1448
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Qy 1509 GTGCTGTGGCGCGTGGCGCTGCTCTGTGCGCGTCCCTTTCTTGTCTGGTGGGCGTCAAG 1568
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Qy 1629 CCTCTCGCTCTGTCGCGCGCTCTCTGCTCTGCGGGGCGCACCGCGCTGCCCCGCGCTCG 1688
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Qy 1689 GGGCCCGAGACCGCGGAGCGCGCGCTGTTCAGCGCGCAATGCGCGCGAGCCCCCGCG 1748
Db 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTCAGCGCGCAATGCGCGCGAGCCCCCGCG 720
Qy 1749 CAGCTGGCGCGCTGCGGTGCTCATGCTGTGGGTCAACCGCGCTACTTCTTCTGCGCTTT 1808
Db 721 CAGCTGGCGCGCTGCGGTGCTCATGCTGTGGGTCAACCGCGCTACTTCTTCTGCGCTTT 780
Qy 1809 CTGTGCTCAGCATCTCTACGGCTCATCGGGCTCATCGGGCGGAGCTGTGGAGACGCGCGCG 1868
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Qy 1869 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACACCGTCCGCGTCTCTG 1928
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Qy 1929 C 1929
Db 901 C 901

RESULT 14
AX572965
LOCUS AX572965 1239 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 1 from Patent WO02057791.
ACCESSION AX572965
VERSION AX572965.1 GI:26005013
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
REFERENCE
AUTHORS Brown,J.P., Burmer,G.C., Roush,C.L. and Kulander,B.G.
TITLE Diagnostic and therapeutic compositions and methods related to gpr
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JOURNAL Patent: WO 02057791-A 1 25-JUL-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
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ORIGIN
Query Match 29.4%; Score 901; DB 6; Length 1239;
Best Local Similarity 100.0%; Pred. No. 2.3e-131;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1029 ATGGCAGCCCTGTGAACCGGACGACCGGCCCGAGGGGCGCGGAGCGCGCGCGCC 1088
Db 1 ATGGCAGCCCTGTGAACCGGACGACCGGCCCGAGGGGCGCGGAGCGCGCGCGCGCC 60
Qy 1089 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGGCTTCCCTGGGGCGCTGTGCGG 1148
Db 61 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGGCTTCCCTGGGGCGCTGTGCGG 120
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Qy 1209 ATGTGTATGGCGCGCTACCGGAGCATGCGGACCAACCACTGTGTACCTGGGAGCATG 1268
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Db 301 TCGCGGCGCTTGGGTGTGGGCGCGTGTCTGCGCGCTGTGCTGTGCGGCGCTGTGCTGT 360
Qy 1389 TGCACCTACGCCACGCTGCTGCACATGACCGGCTGTGACGCTGTGACGCTACCTGGCCATC 1448
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Qy	1629	CCTCTCGCCTCGTCGCGCCTCTCTGGGTCTCTCGCGGCGCCACCGCCGTCCTCCCGCGTCG	1688
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Db	661		720
Qy	1749	CAGCTGGGCGCTGCGTGTCTATGCTGTGGGTCAACCGCCTACTTCTTCTGCGCCTTT	1808
Db	721		780
Qy	1809	CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGAGAGCGCGCGCGG	1868
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Db	841		900
Qy	1929	C 1929	
Db	901	C 901	

Search completed: April 11, 2005, 06:41:16
Job time : 13275.4 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:45:34 ; Search time 5361.1 Seconds
(without alignments)
11198.460 Million cell updates/sec

Title: US-09-719-485-2
Perfect score: 1239
Sequence: 1 atgggcagccctggaacgg.....acgtgaagacgatgggataa 1239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ats.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1239	100.0	1239	6	BD211243	Cloning a
2	1239	100.0	1239	6	CQ724376	Sequence
3	1239	100.0	1239	6	CQ831648	Sequence
4	1239	100.0	1239	6	AX154589	Sequence
5	1239	100.0	1239	6	AX549187	Sequence
6	1239	100.0	1239	6	AX572965	Sequence
7	1239	100.0	1239	9	AY603964	Homo sapi
8	1078	87.0	1390	6	BD211244	Cloning a
9	901	72.7	1161	6	AX154591	Sequence
10	901	72.7	2040	9	AF034632	Homo sapi
11	901	72.7	3066	6	BD211242	Cloning a
12	901	72.7	163284	9	AL137000	Human DNA
13	901	72.7	341560	2	AL596304	Homo sapi
14	901	72.7	349980	6	AX711879	Sequence
15	901	72.7	349980	6	AX739961	Sequence
16	900	72.6	900	6	BD211249	Cloning a
17	592.2	47.8	692	9	HS339407	Homo sapi
18	572.2	46.2	692	9	HS342408	Homo sapi
19	557.4	45.0	615	9	HS339459	Homo sapi

20	424.8	34.3	701	9	HS3326768	AJ326768 Homo sapi
21	340	27.4	602	6	BD211251	BD211251 Cloning a
22	307	24.8	191949	2	AC109158	AC109158 Mus muscu
23	283	22.8	283	6	AR168467	AR168467 Sequence
24	283	22.8	283	6	AR182284	AR182284 Sequence
25	283	22.8	283	6	AR303910	AR303910 Sequence
26	283	22.8	283	6	BD056681	BD056681 Galanin r
27	283	22.8	283	6	BD064652	BD064652 Human gal
28	283	22.8	283	6	BD064664	BD064664 Mouse sapi
29	266.8	21.5	573	9	HS341295	AJ341295 Homo sapi
30	264.8	21.4	1092	6	BD211245	BD211245 Cloning a
31	255.8	20.6	1050	6	BD222611	BD222611 Canine gr
32	255.8	20.6	1050	6	AR429668	AR429668 Sequence
33	244	19.7	1751	5	AB095995	AB095995 Gallus ga
34	242.6	19.6	1351	5	AB095997	AB095997 Gallus ga
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36	242.6	19.6	4121	5	AB095994	AB095994 Gallus ga
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38	234.8	19.0	1101	4	SSU60178	U60178 Sub scrofa
39	233.2	18.8	870	4	SSU60180	U60180 Sub scrofa
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41	231.6	18.7	1095	6	BD221741	BD221741 Mouse gro
42	231.6	18.7	1095	6	AR454841	AR454841 Sequence
43	231.6	18.7	4009	6	BD221740	BD221740 Mouse gro
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45	230	18.6	1029	6	AR156352	AR156352 Sequence

ALIGNMENTS

RESULT 1
BD211243
LOCUS 1239 bp DNA linear PAT 17-JUL-2003
DEFINITION Cloning and identification of motilin receptor.
ACCESSION BD211243
VERSION BD211243.1 GI:33021013
KEYWORDS JP 2002517507-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 1239)
AUTHORS Feighner,S.D., Patchett,A.A., Tan,C., Mckee,K., Macnei,D.,
Howard,A.D., Pong,S.S. and Smith,R.G.
TITLE Cloning and identification of motilin receptor
JOURNAL Patent: JP 2002517507-A 2 18-JUN-2002;
COMMENT MERCK AND CO INC
OS Homo sapiens (human)
PN JP 2002517507-A/2
PD 18-JUN-2002
PF 08-JUN-1999 JP 2000553444
PI 12-JUN-1998 US 60/089098
PI SCOTT D FEIGHNER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI
DOUGLAS MACNEIL,
PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH
PC C07K14/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02, PC
C12N15/00
CC Cloning and identification of motilin receptor. FH Key
Location/Qualifiers
FT source 1. .1239
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ORIGIN

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Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1021 CTGCAACTTTTCTAATCTAGCGCATCTATCAACCCCAATCCTCTAACAACCTCAATTTCAAAG 1080
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RESULT 4

LOCUS AX154589 1239 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 9 from Patent WO0138355.
ACCESSION AX154589
VERSION AX154589.1 GI:14536175
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Sheppard, P. O., Jaspers, S. R., Deisher, T. A. and Bishop, P. D.
AUTHORS Method of forming a peptide-receptor complex with zsig33 and
TITLE therapeutic use thereof
JOURNAL Patent: WO 0138355-A 9 31-MAY-2001;
ZymoGenetics, Inc. (US)

FEATURES

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Best Local Similarity 100.0%; Pred. No. 3.2e-155;
Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGGGAGCCCTCGAAGCGGACGCGCCCGGAGGGGGCGGGAGCGCGCGTGGGCC 60
Qy 61 GCGCTGCGCCTTGGAGAGCGCGCTGCTGCGCCCTTTTCCCTTGGGGCGCTGGTGGC 120
Db 61 GCGCTGCGCCTTGGAGAGCGCGCTGCTGCGCCCTTTTCCCTTGGGGCGCTGGTGGC 120
Qy 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

Qy 181 ATGTGATCGGCGCTACCGGGACATCGGGACCAACCAACTTGTACTCTGGGCGAGCATG 240
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Db 241 GCGGTGTCGACCTACTACTCTGCTCGGGGTGCGGTTCGACCTGTACCGCTCTGGGCG 300
Qy 301 TCGGGCCCTCGGTGTTTGGGGCGCTGCTGTCGGCGCTGTCCTCTACGTGGGCGAGGCG 360
Db 301 TCGGGCCCTCGGTGTTTGGGGCGCTGCTGTCGGCGCTGTCCTCTACGTGGGCGAGGCG 360
Qy 361 TGCACCTACGCCACGCTGCTGCACATGACCGGCTCAGCGTCGAGCGCTACTTGGCCATC 420
Db 361 TGCACCTACGCCACGCTGCTGCACATGACCGGCTCAGCGTCGAGCGCTACTTGGCCATC 420
Qy 421 TCGCGCCCTCGCGCCCGCTTGTGTCAACCGGGCGCGCTCCGCGCGCTCATCGCT 480
Db 421 TCGCGCCCTCGCGCCCGCTTGTGTCAACCGGGCGCGCTCCGCGCGCTCATCGCT 480
Qy 481 GTGCTCTGGGCGGTGGGCGCTGCTCTGTCGGGTCCCTTCTTGTTCCTGGTGGGCTCGAG 540
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Db 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCCACCGGAGAGCGCTCGCGCTCGCTG 900
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[illegible]

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Qy	121	GTGACCGCTGTGCTGTGCTGTTCGTTCGTTCGGGGGTGAGCGCACAAGTGTGTCACCGTG	180
Db	121	GTGACCGCTGTGCTGTGCTGTTCGTTCGTTCGGGGGTGAGCGCACAAGTGTGTCACCGTG	180
Qy	181	ATGCTGATCGGGCGCTACCGGGACATCGGACACCAACCAACTTTGTACCTGGGCGAGCATG	240
Db	181	ATGCTGATCGGGCGCTACCGGGACATCGGACACCAACCAACTTTGTACCTGGGCGAGCATG	240
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Qy	361	TGCACTTACGCCACGCTGTCTGCACATGACCGCGCTCAGCGTCGAGCGCTACTTGGCCCATC	420
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Qy	481	GTGCTCTGGGCGCTGGGCGCTGTCTCTGCGGTCCTTCTTGTTCCTGTGGGCGTCAAG	540
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Qy	781	CTGTGCTCTAGCATCTCTTACGGGCTCATCGGGCGGAGCTGTGGAGAGCGCGCGCGCG	840
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Db	1081	AAGTACAGAGCGCGGCTTTAAACTGTGCTTCGCAAGGAAGTCCAGGCGAGAGGCTTC	1140
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DEFINITION	Human sapiens motilin/ghrelin receptor mRNA, complete cds.		
ACCESSION	AY603964		
VERSION	AY603964.1	GI:47571310	
KEYWORDS			
SOURCE	Human sapiens (human)		
ORGANISM	Human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1. (bases 1 to 1239)		
TITLE	King, M.M., Aronstam, R.S. and Sharma, S.V.		
JOURNAL	Isolation of cDNA coding for motilin/ghrelin receptor (MTLr1/GPR38)		
REFERENCE	2. (bases 1 to 1239)		
AUTHORS	King, M.M., Aronstam, R.S. and Sharma, S.V.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-APR-2004) Guthrie cDNA Resource Center, Guthrie Foundation, 1 Guthrie Square, Sayre, PA 16840, USA		
FEATURES	Location/Qualifiers		
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Db	181	ATGCTGATCGGGCGCTACCGGACATCGGACACACCAACCTTGTACCTGGGACGATG	240
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LOCUS	BD211244			
DEFINITION	Cloning and identification of motilin receptor.			
ACCESSION	BD211244			
VERSION	BD211244.1	GI:33021014		
KEYWORDS	JP 2002517507-A/3.			

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1390)
AUTHORS	Feigner,S.D., Patchett,A.A., Tan,C., Mckee,K., Macnei,D., Howard,A.D., Pong,S.S. and Smith,R.G.
TITLE	Cloning and identification of motilin receptor
JOURNAL	Patent: JP 2002517507-A 3 18-JUN-2002; MERCK AND CO INC
COMMENT	OS Homo sapiens (human) PN JP 2002517507-A/3 PD 18-JUN-2002 PF 08-JUN-1999 JP 2000553444 PR 12-JUN-1998 US 60/089098 PI SCOTT D FEIGNER,ARTHUR A PATCHETT,CARINA TAN,KAREN MCKEE,PI DOUGLAS MACNEIL, PI ANDREW D HOWARD,SHENG SHUNG PONG,ROY G SMITH PC C07K14/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02,PC C12N15/00
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VERSION	AF034632.1	GI:2654158			
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ORGANISM	Homo sapiens				
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AUTHORS	McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D., Hreniuk,D.L., Smith,R.G., Howard,A.D. and Van der Ploeg,L.H.				
TITLE	Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue and neurotensin receptors				
	Genomics 46 (3), 426-434 (1997)				
JOURNAL	98110578				
MEDLINE	9441746				
PUBMED					
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AUTHORS	McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D., Hreniuk,D.L., Smith,R.G., Van Der Ploeg,L.H.T. and Howard,A.D.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co., Inc., PO Box 2000, Rahway, NJ 07065, USA				
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ORIGIN

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LOCUS

LOCUS BT208

LOCUS BT208

BD211242

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DNA

linear

PAT 17-JUL-2003

The true right end of clone RP11-103J18 is at 163284 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-203J16 is from the library RP11-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 Zhang, Y., Mofatt, M., Cookson, W. and Tinsley, J.O.			
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REFERENCE 1

AUTHORS Zhang, Y., Moffatt, M. and Cookson, W.
 TITLE Treatment and diagnosis of B cell chronic lymphocytic leukaemia
 JOURNAL Patent: WO 03000296-A 1 03-JAN-2003;
 ISIS INNOVATION LIMITED (GB)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%

Maximum Match 100%

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1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2155	100.0	412	1	MTLR_HUMAN	O43193 homo sapien
2	907	42.1	363	2	O93413	O93413 spherooides
3	895	41.5	385	2	O6YGG3	O6YGG3 acanthopagr
4	864.5	40.1	366	1	GHSR_PIG	O95254 sus scrofa
5	863.5	40.1	366	1	GHSR_HUMAN	O92847 homo sapien
6	863	40.0	360	2	O6B7N9	O6B7N9 macaca fasc
7	861.5	40.0	364	1	GHSR_MOUSE	O99P50 mus musculus
8	861.5	40.0	364	1	GHSR_RAT	O08725 rattus norv
9	855	39.7	347	2	O72T14	O72T14 gallus gall
10	851.5	39.5	374	2	O93412	O93412 spherooides
11	825.5	38.3	366	2	O8MHZ5	O8MHZ5 oris aries
12	759	35.2	331	2	O7ZJZ9	O7ZJZ9 gallus gall
13	671	31.1	295	2	O6YGG2	O6YGG2 acanthopagr
14	643	29.8	267	2	O7ZJZ8	O7ZJZ8 gallus gall
15	608	28.2	559	2	O93414	O93414 spherooides
16	535	24.8	211	2	O711Q8	O711Q8 gallus gall
17	501	23.2	424	1	NTR1_RAT	P20789 rattus norv
18	499.5	23.2	424	1	NTR1_MOUSE	O88319 mus musculus
19	497	23.1	418	1	NTR1_HUMAN	P30989 homo sapien
20	487.5	22.6	426	2	O8NE20	O8NE20 homo sapien
21	485.5	22.5	215	2	O711Q7	O711Q7 gallus gall
22	485.5	22.5	403	2	O7LDP6	O7LDP6 homo sapien
23	485.5	22.5	426	2	O9HB89	O9HB89 homo sapien
24	478.5	22.2	395	2	O91Z76	O91Z76 mus musculus
25	478.5	22.2	395	2	O8BZ39	O8BZ39 mus musculus
26	477.5	22.2	395	2	O9JIB1	O9JIB1 rattus norv
27	477	22.1	415	2	O96AM5	O96AM5 homo sapien
28	476	22.1	412	2	O7LC54	O7LC54 homo sapien
29	476	22.1	415	2	O9GZQ4	O9GZQ4 homo sapien
30	475.5	22.1	395	2	O9ESQ4	O9ESQ4 rattus norv
31	474.5	22.0	493	2	O7RTK4	O7RTK4 anopheles g

RESULT 1

MTLR_HUMAN

ID MTLR_HUMAN STANDARD; PRT; 412 AA.

AC O43193;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE 25-OCT-2004 (Rel. 45, Last annotation update)

DE Motilin receptor (G protein-coupled receptor 38).

GN Name=MLNR; Synonyms=GPR38, MTLR, MTLR1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM A).

RX MEDLINE=98110578; PubMed=9441746; DOI=10.1006/geno.1997.5069;

RA McKee K.K., Tan C.P., Palya O.C., Liu J., Feighner S.D.,

RA Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;

RT "Cloning and characterization of two human G protein-coupled receptor

genes (GPR38 and GPR39) related to the growth hormone secretagogue and

neurotensin receptors.";

RL Genomics 46:426-434(1997).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS A AND B).

RX MEDLINE=99316084; PubMed=10381885; DOI=10.1126/science.284.5423.2184;

RA Feighner S.D., Tan C.P., McKee K.K., Palya O.C., Hreniuk D.L.,

RA Pong S.-S., Austin C.P., Figueroa D., MacNeil D., Cascieri M.A.,

RA Nargund R., Bakshi R., Abramovitz M., Stocco R., Kargman S.,

RA O'Neill G., van der Ploeg L.H.T., Evans J., Patchett A.A., Smith R.G.,

RA Howard A.D.;

RT "Receptor for motilin identified in the human gastrointestinal

system.";

RL Science 284:2184-2188(1999).

RN [3]

RP SEQUENCE FROM N.A.

RX PubMed=15057823; DOI=10.1038/nature02379;

RA Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,

RA Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,

RA Ainscough R., Almeida J.P., Ambrose K.D., Keenan S.J., Oliver K., Scott C.E.,

RA Ashwell R.I.S., Babbage A.K., Baguley C.L., Bailey J., Bannerjee R.,

RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,

RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M.,

RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,

RA Deloukas P., Dhumi P., Dunham I., Dunn M., Earthrow M.E.,

RA Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,

RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,

RA Grafham D.V., Gribble S.M., Griffiths C., Hall R.E., Hammond S.,

RA Harley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,

RA Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,

RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamornratt D.A.,

RA Lloyd D.M., Lloyd C., Loveland J.B., Lovell J., Martin S.,

RA Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,

RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
RA Sehra H.K., Showkeen R., Skuce C.D., Smith M., Steward C.A., Tubby B.,
RA Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A.,
RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,
RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
RT "The DNA sequence and analysis of human chromosome 13.",
RL Nature 428:522-528(2004).
RN [4]
RP FUNCTION.
RX MEDLINE=21219832; PubMed=1132507; DOI=10.1385/ENDO.14:1.009;
RA Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D.,
RA Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.;
RA "Growth hormone secretagogue receptor family members and ligands.",
RT Endocrine 14:9-14(2001).
RL
CC -!- FUNCTION: Receptor for motilin.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=O43193-1; Sequence=Displayed;
CC Name=B;
CC IsoId=O43193-2; Sequence=VSP_001894;
CC -!- TISSUE SPECIFICITY: Expressed only in thyroid, stomach, and bone
marrow.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; AF034632; AAC26081.1; -;
CC EMBL; AL1137000; CAC19107.1; -;
CC Genew; HGNC:4495; MLNR.
CC MIM; 602885; -;
CC GO; GO:0005987; C:integral to plasma membrane; TAS.
CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
CC GO; GO:0007586; P:digestion; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; TAS.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G PROTEIN RECP FL_1; 1.
CC PROSITE; PS00262; G PROTEIN RECP FL_2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW Transmembrane.
FT DOMAIN 1 35 Extracellular (Potential).
FT TRANSMEM 36 56 1 (Potential).
FT DOMAIN 57 74 Cytoplasmic (Potential).
FT TRANSMEM 75 94 2 (Potential).
FT DOMAIN 95 112 Extracellular (Potential).
FT TRANSMEM 113 134 3 (Potential).
FT DOMAIN 135 157 Cytoplasmic (Potential).
FT TRANSMEM 158 178 4 (Potential).
FT DOMAIN 179 246 Extracellular (Potential).
FT TRANSMEM 247 270 5 (Potential).
FT DOMAIN 271 298 Cytoplasmic (Potential).
FT TRANSMEM 299 320 6 (Potential).
FT DOMAIN 321 334 Extracellular (Potential).
FT TRANSMEM 335 358 7 (Potential).
FT DOMAIN 359 412 Cytoplasmic (Potential).
FT DISULFID 111 235 By similarity.
FT CARBOHYD 6 6 N-linked (GlcNAc. . .) (Potential).
FT FT 192 N-linked (GlcNAc. . .) (Potential).
FT VARSPLIC 301 LVVLAFLICWLPFHVGRRIYINTEDSRMVFSQYFNIVAL
SRDTAGEVADTGDTGVGTETSAANVKTWG -> RKWSRRG
SKDACIQSAPPGTAQTGLPLLAQLWAPLPAPFPISAPAS

FT TRRGSGGIYNNLVALPRWQHLKHGRFADDDLLSVL
FT (in isoform B).
FT /FTId=VSP_001894.
SQ SEQUENCE 412 AA; 45344 MW; CL3PF6165012DEF3 CRC64;
Query Match 100.0%; Score 2155; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 9.4e-135;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPPLGALVPVTAVCCLFVVGVSGNVTV 60
Db 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPPLGALVPVTAVCCLFVVGVSGNVTV 60
Qy 61 MLIGRYDMRTTNTLYLGSMVAVSDLLILGLPFDFLYLRWSRPWVFGPLLCRLSLYYVGE 120
Db 61 MLIGRYDMRTTNTLYLGSMVAVSDLLILGLPFDFLYLRWSRPWVFGPLLCRLSLYYVGE 120
Qy 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVALIAVLMAVALLSAGPFLVGV 180
Db 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVALIAVLMAVALLSAGPFLVGV 180
Qy 181 QDPGISVVGNGTARTIASSPLASSPPLWLSRAPPSPPSPETAEEAALFSRRCRSPA 240
Db 181 QDPGISVVGNGTARTIASSPLASSPPLWLSRAPPSPPSPETAEEAALFSRRCRSPA 240
Qy 241 QLGALRVMLVWTYAYFFLPFLCLISILYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300
Db 241 QLGALRVMLVWTYAYFFLPFLCLISILYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300
Qy 301 LVVLAFLICWLPFHVGRRIYINTEDSRMVFSQYFNIVALQLFYLSASINPIYLNLSK 360
Db 301 LVVLAFLICWLPFHVGRRIYINTEDSRMVFSQYFNIVALQLFYLSASINPIYLNLSK 360
Qy 361 KYRAAFAKLLARKSRPRGHSRDTAGEVADTGDTGVGTETSAANVKTWG 412
Db 361 KYRAAFAKLLARKSRPRGHSRDTAGEVADTGDTGVGTETSAANVKTWG 412
RESULT 2
O93413 PRELIMINARY; PRT; 363 AA.
ID O93413
AC O93413
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Orphan G protein-coupled receptor.
OS Spheroidea nephelus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Spheroidea.
OX NCBI_TaxID=39110;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20092336; PubMed=10628755; DOI=10.1210/me.14.1.160;
RX Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,
RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Margund R.,
RA Patchett A.A., Howard A.D., Smith R.G.;
RT "Ligand activation domain of human orphan growth hormone (GH)
secretagogue receptor (GHS-R) conserved from Pufferfish to humans.";
RT Mol. Endocrinol. 14:160-169(2000).
RL -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF082210; AAC33473.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.

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DR PRINTS; PR00237; GPCRHHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_1; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 363 AA; 41324 MW; 74518BD9CD310991 CRC64;

Query Match 42.1%; Score 907; DB 2; Length 363;
Best Local Similarity 50.6%; Pred. No. 3e-52;
Matches 180; Conservative 56; Mismatches 76; Indels 44; Gaps 5;

QY 31 SPFGALVPTVAVCLCLFVGVGCVGVTMLIGRYDMRTTNLYLGSMAVSDLLILLG 90
DB 31 SLPFASLTIPVTCILFVGVGTNTMTILIQYFKOMKTTNLYLGSMAVSDLVFLC 90

QY 91 LPFDLYLRWSRPWFGPCLRLSLYGVGGCTYATLLHMTALSVERYLAICRPLRVLV 150
DB 91 LPFDLYLRWKYVPLFGEAVCLYHYIFEGCTSAITLHMTALSVERYLAISPLASKV 150

QY 151 TRRRVRLIYVAVALLSAGFLVGVGQDPGIVVPLGNGTARIASSPIASSPPLWL 210
DB 151 TRRRVQYIILALWCFALVSAAPTFLVGVGYD-----NET----- 185

QY 211 SRAPPSPPSPETAEEAALFSECRPSPAQL--GALRVMLVMTTAYRFLPCLLSILY 268
DB 186 ----HPDNTG-----QCKTYALSSQGLHIMVSTYFFCPMLCLFLY 229

QY 269 LIGRELSSRRPLRGAASGRGRHRQTVRVLLVVLVLAFLIICWLPFHVGRIIYNT 328
DB 230 SIGCKLWKSNDLQGPCALARESHRQTVKILVVVLAFLIICWLPYHIGRNLFAQ 289

QY 329 MMYFSQYFNIVALQFYLSASINPILYLIISKYRAAFAFKLLARKSRPRGRHRS 384
DB 290 TAMLSONFNMAVMVLCYLSASINPVVYMLMSRYRAAKRLLHQ-RPKPAHRQ 344

RESULT 3
Q5IGZ3
AC Q6YGZ3; PRELIMINARY; PRT; 385 AA.
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Growth hormone secretagogue receptor la.
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI_TaxID=72011;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15062547; DOI=10.1016/j.mce.2003.11.020;
RA Chan C.B., Cheng C.H.K.;
RT "Identification and functional characterization of two alternatively
spliced growth hormone secretagogue receptor transcripts from the
pituitary of black seabream Acanthopagrus schlegelii."
RL Mol. Cell. Endocrinol. 214:81-95(2004).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY151040; AAN77875.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . . IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.
DR InterPro; IPR0033905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCRHHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_1; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.

SQ SEQUENCE 385 AA; 43697 MW; 665CBDA9702887A9 CRC64;
Query Match 41.5%; Score 895; DB 2; Length 385;
Best Local Similarity 45.7%; Pred. No. 2e-51;
Matches 191; Conservative 62; Mismatches 99; Indels 66; Gaps 11;

QY 17 PFWPALPPCDERRCS-----PPFLG-----ALVPVTAVCLCLFVGVGSGNV 57
DB 2 PSWPNLSECLSLNCSWEETRNRATKFDGLPLPLNYYSIPLLTGITIACTLLFLVGVAGNV 61

QY 58 VTVMILIGRYDMRTTNLYLGSMAVSDLLILLGPPFDLYLRWSRPWFGPCLRLSLYV 117
DB 62 MTLVVSRYDMRTTNLYLGSMAVSDLLIFLCPLDLYRMWRYRPFWDGDKLFOFV 121

QY 118 GEGCTYATLLHMTALSVERYLAICRPLRVLVTRRRVRLIYVAVALLSAGPFLPLV 177
DB 122 SESCTYSTILITALSVERYLAICFPLRAKALVTKERVALLLLMTVYLLSAGPFFV 181

QY 178 GVEQD---PGISVVPGLNGTARIASSPIASSPPLWLSRAPPPSPGSPETAEEAALF 234
DB 182 GVERDSMMPGNLSWVGNGTGFF-----PEEGD-----TRE 212

QY 235 CRPS--PAQLGALRVMLVMTTAYRFLPCLLSILYGLIGRELSSRRPLR-GPAASGR 291
DB 213 CKMTHYAVESGUMGANVWLSVFFPMPVFCUTVLSLIGRLWQHRRTNINSRVHREK 272

QY 292 GHRQTVRVLLVVLVLAFLIICWLPFHVGRIIYNTEDS---RMVFSQYFNIVALQFYLSA 348
DB 273 SNRQTIKMLVVVLAFLVCLWLPFHVGRLQFRLSDAPSLLSLSEYCSLVSVVLYLSA 332

QY 349 SINPILYLIISKYRAAFAFKLL-LARKSRPRGRHRSRDAGEVAGDTGGDTVGYTETS 405
DB 333 AINPILYINMSKRYGAARLFGLIDSQPRG-----RTASTVKGDGNS---GMTST 382

RESULT 4
GHSR_PIG
ID GHSR_PIG STANDARD; PRT; 366 AA.
AC Q95254; Q95255;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
peptide receptor) (GHRP) (ghrelin receptor).
GN Name=GHSR;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RX STRAIN=Yorkshire; TISSUE=Pituitary;
RX MEDLINE=96337998; PubMed=8688086;
RA Howard A.D., Feighner S.D., Cully D.F., Arena J.P., Liberato P.A.,
Rosenblum C.I., Hamelin M., Hreniuk D.L., Palyha O.C., Anderson J.,
Pares P.S., Diaz C., Chou M., Liu K.K., McKee K.K., Pong S.-S.,
Chang L.-Y., Elbrecht A., Dashkevich M., Heavens R., Rigby M.,
Sirinathsinghji D.J.S., Dean D.C., Melillo D.G., Patchett A.A.,
Nargund R., Griffin P.R., Demartino J.A., Gupta S.K., Schaeffer J.M.,
Smith R.G., van der Ploeg L.H.T.;
RT "A receptor in pituitary and hypothalamus that functions in growth
hormone release."
RL Science 273:974-977(1996).
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
stimulates growth hormone secretion. Binds also other growth
hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
as well as non-peptide, low molecular weight secretagogues (e.g.
L-692,429, MK-0677, adenosine).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1A;
IsoId=Q95254-1; Sequence=Displayed;

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Db 213 IFFFLPVCLTVLYSLGKLRERRRDAVVCASLRDQNHQTVKMLAVVVFATLCLWP 272
Qy 314 PHVGRIIYNTEDS---RMVFSQVFNIALQLFVLSASINPILNLSKRYRAAFKL 370
Db 273 PHVGRYLSKSPGSLGSLAQISQYCNLSFVLFYLSAANPILNLSKRYRAAFRL 332
Qy 371 LARKSRPRGFRHSRTAGEVAGDTGDTVGVGTETSAN 407
Db 333 GFEPFSQRKSLTKDESSR-----AMTESSIN 359

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RESULT 7

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CHSR_MOUSE
ID CHSR_MOUSE STANDARD; PRT; 364 AA.
AC Q99P50; QB8WX9; Q91282;
DT 28-FEB-2003 (Rel. 41, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
DE peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=Ghsr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kandi A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konggaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE OF 1-183 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RA Kacsoh B.;
RT "Cloning of mouse ghrelin/growth hormone secretagogue receptor cDNA by
RT rapid amplification of cDNA ends (RACE).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 73-257 FROM N.A.
RC STRAIN=129Sv1mJ;
RA Peng X., Frohman L.A., Kineman R.D.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth

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CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692,429, MK-0677, adenosine) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: AK049671; BAC33866.1; -
CC EMBL: AY056474; AAL13336.1; -
CC EMBL: AF332997; AAG61141.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS: PR00237; GPCRHHODOPS.
CC PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Transmembrane.
CC DOMAIN 1 40 Extracellular (Potential).
CC TRANSMEM 41 66 1 (Potential).
CC DOMAIN 67 72 Cytoplasmic (Potential).
CC TRANSMEM 73 96 2 (Potential).
CC DOMAIN 97 117 Extracellular (Potential).
CC TRANSMEM 118 139 3 (Potential).
CC DOMAIN 140 162 Cytoplasmic (Potential).
CC TRANSMEM 163 183 4 (Potential).
CC DOMAIN 184 211 Extracellular (Potential).
CC TRANSMEM 212 235 5 (Potential).
CC DOMAIN 236 263 Cytoplasmic (Potential).
CC TRANSMEM 264 285 6 (Potential).
CC DOMAIN 286 302 Extracellular (Potential).
CC TRANSMEM 303 326 7 (Potential).
CC DOMAIN 327 364 Cytoplasmic (Potential).
CC DISULFID 115 197 By similarity.
CC CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 187 187 N-linked (GlcNAc...) (Potential).
CC CONFLICT 59 59 G -> S (in Ref. 2).
CC SEQUENCE 364 AA; 40969 MW; 8F1214E58EF3B2E8 CRC64;
SQ
Query Match 40.0%; Score 861.5; DB 1; Length 364;
Best Local Similarity 48.3%; Pred No. 3.1e-49;
Matches 185; Conservative 52; Mismatches 81; Indels 65; Gaps 11;
Qy 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPFLGALVPVTAVCLFVGVGSG 55
Db 2 WNAT--PSEEPENVTLDLDWDASPGNDSLSDELPLFPAPLLAGVTATCAVLFVGVISG 59
Qy 56 NVVTVMILGRVDRMTTNLYLGMVSDLLILGLPDLVRLWRSRPMVGPILCRSL 115
Db 60 NLLTMLVVSRELRFTTNLYLSSMAFSDLLIFLCPLDLVRLWQYRPNWFGDLCFLQ 119
Qy 116 YVGECTVATLLHMTALSVRYLAICRPLRVLVTRRRVRLAVLWAVALLSAGPFLF 175
Db 120 FVSECTVATVLTITALSVERYFAICPLRAKVVTKGVKVLIVLWAVAFCSAGPIFV 179
Qy 176 LVGVEQDPGISVWFGNLNGTARIASSPLASSPPLMLSRAPPPSPGPTBAALFSPREC 235
Db 180 LVGVEHE-----NCT-----DPRD-----TNEC 197
Qy 236 RPS--PAQLGALRVLMTWTATYFPLCLSLYLIGLELWSSRRPRGPAASG---RE 290
Db 198 RATEFAVRSGLLTVMWVSSVFFFLPVFLVLYSLIGKRLW--RR--RGOAVGSSLRD 253
Qy 291 RGHQTVRVLLVVLAFIICWLPHFVGRIIYNTEDS---RMVFSQVFNIALQLFVLS 347
Db 254 QNHKQTVKMLAVVVFATLCLWLPFHVGRYLSKSPGSLGTAQISQYCNLSVFLVFLYLS 313

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QY 348 ASINPILYNLSKKYRAAFKLL 370
Db 314 AAINPILYNLSKKYRAAFKLL 336

RESULT 8
CHSR_RAT
ID CHSR_RAT STANDARD; PRT; 364 AA.
AC O08725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=Ghsr;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=9724555; PubMed=902793; DOI=10.1210/me.11.4.415;
RA McKee K.K., Palyha O.C., Feighner S.D., Hreniuk D.L., Tan C.P., Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.;
RT "Molecular analysis of rat pituitary and hypothalamic growth hormone secretagogue receptors.";
RL Mol. Endocrinol. 11:415-423(1997).
RN [2]
RP SEQUENCE OF 1-240 FROM N.A.
RC STRAIN=Wislat; TISSUE=Pituitary;
RX MEDLINE=98100386; PubMed=9437732; DOI=10.1016/S0196-9781(97)00263-5;
RA Yokote R., Sato M., Matsubara S., Ohye H., Nimmi M., Murao K., Takahara J.;
RT "Molecular cloning and gene expression of growth hormone-releasing peptide receptor in rat tissues.";
RL Peptides 19:15-20(1998).
RN [3]
RP FUNCTION.
RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";
RL Nature 402:656-660(1999).
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins. Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6) as well as non-peptide, low molecular weight secretagogues (e.g. L-692,429, MK-0877, adenosine) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC
CC EMBL; U94321; AAC53156.1; -;
CC RGD; AB001982; BAA31777.1; AUT_INIT.
CC RBL; 621397; Ghsr.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1.1;
CC PRINTS; PR00237; GPCRHOODPSN.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 40 Extracellular (Potential).
FT TRANSMEM 41 66 1 (Potential).
FT DOMAIN 67 72 Cytoplasmic (Potential).
FT TRANSMEM 73 96 2 (Potential).

FT DOMAIN 97 117 Extracellular (Potential).
FT TRANSMEM 118 139 3 (Potential).
FT DOMAIN 140 162 Cytoplasmic (Potential).
FT TRANSMEM 163 183 4 (Potential).
FT DOMAIN 184 211 Extracellular (Potential).
FT TRANSMEM 212 235 5 (Potential).
FT DOMAIN 236 263 Cytoplasmic (Potential).
FT TRANSMEM 264 285 6 (Potential).
FT DOMAIN 286 302 Extracellular (Potential).
FT TRANSMEM 303 326 7 (Potential).
FT DOMAIN 327 364 Cytoplasmic (Potential).
FT DISULFID 115 197 By similarity.
FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 187 187 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 364 AA; 40963 MW; DCBF559BE061EE8 CRC64;

Query Match 40.0%; Score 861.5; DB 1; Length 364;
Best Local Similarity 48.3%; Pred. No. 3.1e-49;
Matches 185; Conservative 52; Mismatches 81; Indels 65; Gaps 11;

QY 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPPLGALVPVTAVCICLFLVGVSG 55
Db 2 WNAI--PSEEPNVTLDLDWDASPGNSLDPDELLPLFPAPLLAGVTATCVAFVVGISG 59
QY 56 NVVTMLIGRYDRMTTNTNLVLSMAVSDLLILGLPFDLYLRWSRPWFGPILCRSL 115
Db 60 NLTLMLVVSFRPRELTNTNLVLSMAVSDLLIFLCMLDLVRLWQYRPWNEFDLLCKLFQ 119
QY 116 YVGECTYATLLHMTALSVRYLAICPLARVAVTRRRVPAALAVLWALLSNGPLF 175
Db 120 FVSECTYATVLTITSLVSRYFAICPLRAKVVTTRGRVKLVILVIMAVAFCSAGPIFV 179
QY 176 LVGVEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPPSGPETAEEAALFSREC 235
Db 180 LVGVEH-----NGT-----DPRD-----TNEC 197
QY 236 RPS--PAQLGALRYMLVMTTAYFPFLPCLISILYGLIGRELWSSRRPLRGPAAG--RE 290
Db 198 RATEFAVRSGLLTVMWVSSVFFPLPVFLCTLVLSYIGRKLW--RR--RGDAAVGASLRD 253
QY 291 RGHRTQTVLLVVLVLAIIICWLPFHVGRIIYINTEDS----RMVYFSQYFNVALQLFVLS 347
Db 254 QNHKQTVMLAVVVFVAFILCWLPHVGRIYLFKSFEPGSEIAQISQYCNLVSVFLVYLS 313
QY 348 ASINPILYNLSKKYRAAFKLL 370
Db 314 AAINPILYNLSKKYRAAFKLL 336

RESULT 9
Q7ZT14
ID Q7ZT14 PRELIMINARY; PRT; 347 AA.
AC Q7ZT14;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Growth hormone secretagogue receptor type 1a.
GN Name=Ghsr; Synonyms=Gharla;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Kidney, and Pituitary;
RX MEDLINE=22874039; PubMed=14511992; DOI=10.1016/S0016-6480(03)00247-8;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Ohta Y., Tsuchida N., Wakita M., Shimada K.;
RT "Molecular characterization of chicken growth hormone secretagogue receptor gene.";
RL Gen. Comp. Endocrinol. 134:198-202(2003).


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DR GO: 0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR003905; GH51 receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01417; GH51RECEPTOR.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; transmembrane.
KW G-protein coupled receptor; Receptor; transmembrane.
SQ SEQUENCE 295 AA; 33883 MW; E7397DCAEDF73873 CRC64;

Query Match 31.1%; Score 671; DB 2; Length 295;
Best Local Similarity 45.3%; Pred. No. 1e-36;
Matches 140; Conservative 43; Mismatches 72; Indels 54; Gaps 7;

QY 17 PWPALPPCDERRCS-----PPPLG-----ALVPVAVCLFVVGSGNV 57
DB 2 PWPNLSECLNSWEETRNRKFDLGLPLPNYSIPLLTGITIACTLLFLVGAGNV 61
QY 58 VTMVLIGRYDRMTTNLYLGSMAVSDLLILGLPDLVRLWRSPVFGPLLCRLSLV 117
DB 62 MTLVVKRYDRMTTNLYLGSMAVSDLLIFLQMPDLVRLWRSPVFGPLLCRLSLV 121
QY 118 GEGCTATLHMTALSVRYLAICPLRARVLVTRRRVRLALIAVLWALLSAGPFLV 177
DB 122 SSSCTVSTILSALTALSVRYLAICPLRAKALVTRRRVRLALIAVLWALLSAGPFLV 181
QY 178 GVEQD---PGISVVGCLNGTARIASPLSPPLWLSRAPPSPSPGPTAAALFSRE 234
DB 182 GVERDSMVFNLISWVGNGTGF-----PEEGD-----TRE 212
QY 235 CRPS--PAQGLARVLMVLTATYFFLPFLCLSLYLGLIGRELWSSRRPLR-GPAASGR 291
DB 213 CKMTHYAVESGLMGAMVLSVFFFPVCLVLSLGRLLQHRHETNINSRVAREK 272
QY 292 GHRQTVRL 300
DB 273 SNRQIKML 281

RESULT 14
Q72ZJ8 PRELIMINARY; PRT; 267 AA.
AC Q72ZJ8
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type 1b.
GN Name=Gharib;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Pituitary;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Wakita M., Shimada K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB095997; BAC76446.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0016520; F: growth hormone-releasing hormone receptor a. . .; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR003905; GH51 receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01417; GH51RECEPTOR.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.

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DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; transmembrane.
SQ SEQUENCE 267 AA; 30209 MW; 00563690B35AD107 CRC64;

Query Match 29.8%; Score 643; DB 2; Length 267;
Best Local Similarity 43.4%; Pred. No. 6.5e-35;
Matches 124; Conservative 58; Mismatches 54; Indels 50; Gaps 5;

QY 33 PFLGALVEPTAVCLFVVGSGNVVTVMLIGRYDRMTTNLYLGSMAVSDLLILGLP 92
DB 19 FPAPVLGTITVACVLLFVVGVLNMTLWVSFRDMRTTNLYLGSMAVSDLLIFLCP 78
QY 93 FDLVLRSPVWVFGPLLCRLSLVVGECVTATLHMTALSVRYLAICPLRARVLVTR 152
DB 79 LDFRLMQYRPNFQDGLLCKLFQFISSECTYSTINLTALSVRYLAICPLRARVIITK 138
QY 153 RRVRLALIAVLWALLSAGPFLVVGVEQDPSGVVPGCLNGTARIASPLSPPLWLSR 212
DB 139 RKVKLVILLWAVSFISAGPIFVLVGEHE-----NGT-----NPLSTN----- 177
QY 213 APPSPSPGPTAAALFSRECPSPAQL--GALRVLMVLTATYFFLPFLCLSLYLGLI 270
DB 178 -----ECRATEYAIRSGLLTMMWISSIFFFLPVFLVCLVLSLI 216
QY 271 GRELWSSRRPLRGPAASGRERHQTIVRL-----LVVLAFLIIC 310
DB 217 GRKLWRRKKNIGPSTIIRKNNKQTVKMLGMAPRALCLQVRVLVC 262

RESULT 15
O93414 PRELIMINARY; PRT; 559 AA.
AC O93414
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Orphan G protein-coupled receptor.
OS Spherooides nephelus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Spherooides.
OX NCBI_TaxID=39110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092336; PubMed=10628755; DOI=10.1210/me.14.1.160;
RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,
RA Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nargund R.,
RA Patchett A.A., Howard A.D., Smith R.G.;
RT "Ligand activation domain of human orphan growth hormone (GH)
secretagogue receptor (GHS-R) conserved from Pufferfish to humans.";
RL Mol. Endocrinol. 14:160-169(2000).
DR EMBL; AF082211; AAC33474.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 559 AA; 61956 MW; AFB9F35FAF0CD5F6 CRC64;

Query Match 28.2%; Score 608; DB 2; Length 559;
Best Local Similarity 29.7%; Pred. No. 2.6e-33;
Matches 156; Conservative 65; Mismatches 124; Indels 180; Gaps 12;

QY 22 LPPCDERRC---SPFLGALVPVTVAVCLFVVGSGNVVTVMLIGRYDRMTTNLYLGL 78
DB 20 LHKCSNOECHWEPV-FGMIVCVTIYIPLMLFGLNLTILVWLPYRMSSTLYLS 78

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:45:34 ; Search time 6014.47 Seconds
(without alignments)
11198.460 Million cell updates/sec

Title: US-09-719-485-4
Perfect score: 1390
Sequence: 1 atggcgagccctggaacgg.....acgtgaagacgatgggataa 1390

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1390	100.0	1390	6	BD211244	BD211244 Cloning a
2	1161	83.5	1161	6	AX154591	AX154591 Sequence
3	1078	77.6	1239	6	BD211243	BD211243 Cloning a
4	1078	77.6	1239	6	CQ724376	CQ724376 Sequence
5	1078	77.6	1239	6	CQ831848	CQ831848 Sequence
6	1078	77.6	1239	6	AX154589	AX154589 Sequence
7	1078	77.6	1239	6	AX549187	AX549187 Sequence
8	1078	77.6	1239	6	AX572965	AX572965 Sequence
9	1078	77.6	1239	9	AV603964	AV603964 Homo sapi
10	1052	75.7	2040	9	AF034632	AF034632 Homo sapi
11	1052	75.7	163284	9	AL137000	AL137000 Human DNA
12	1052	75.7	341560	2	AL596304	AL596304 Homo sapi
13	1052	75.7	349980	6	AX711879	AX711879 Sequence
14	1052	75.7	349980	6	AX739961	AX739961 Sequence
15	1038	74.7	3066	6	BD211242	BD211242 Cloning a
16	900	64.7	900	6	BD211249	BD211249 Cloning a
17	592.2	42.6	692	9	HSA339407	AJ339407 Homo sapi
18	572.2	41.2	692	9	HSA342408	AJ342408 Homo sapi
19	557.4	40.1	615	9	HSA339459	AJ339459 Homo sapi

20	424.8	30.6	701	9	HSA326768	AJ326768 Homo sapi
21	338	24.3	602	6	BD211251	BD211251 Cloning a
22	307	22.1	191949	2	AC109158	AC109158 Mus muscu
23	283	20.4	283	6	AR168467	AR168467 Sequence
24	283	20.4	283	6	AR182284	AR182284 Sequence
25	283	20.4	283	6	AR303910	AR303910 Sequence
26	283	20.4	283	6	BD056681	BD056681 Galanin r
27	283	20.4	283	6	BD064652	BD064652 Human gal
28	283	20.4	283	6	BD064664	BD064664 Mouse gal
29	266.8	19.2	573	9	HSA341295	AJ341295 Homo sapi
30	248.2	17.9	1050	6	BD222611	BD222611 Canine gr
31	248.2	17.9	1050	6	AR429668	AR429668 Sequence
32	242.6	17.5	1351	5	AB095997	AB095997 Gallus ga
33	242.6	17.5	1703	5	AB095996	AB095996 Gallus ga
34	242.6	17.5	1751	5	AB095995	AB095995 Gallus ga
35	242.6	17.5	4121	5	AB095994	AB095994 Gallus ga
36	234.8	16.9	1063	6	AR156351	AR156351 Sequence
37	234.8	16.9	1101	4	SSU60178	U60178 Sus scrofa
38	233.2	16.8	870	4	SSU60180	U60180 Sus scrofa
39	231.6	16.7	1095	6	BD221741	BD221741 Mouse gro
40	231.6	16.7	1095	6	AR454841	AR454841 Sequence
41	231.6	16.7	4009	6	BD221740	BD221740 Mouse gro
42	231.6	16.7	4009	6	AR454840	AR454840 Sequence
43	230	16.5	11029	6	AR156352	AR156352 Sequence
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LOCUS BD211244 1390 bp DNA linear PAT 17-JUL-2003
DEFINITION Cloning and identification of motilin receptor.
ACCESSION BD211244
VERSION BD211244.1 GI:33021014
KEYWORDS JP 2002517507-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (Bases 1 to 1390)
AUTHORS Feighner,S.D., Patchett,A.A., Tan,C., Mckee,K., Macneil,D.,
Howard,A.D., Pong,S.S. and Smith,R.G.
TITLE Cloning and identification of motilin receptor
JOURNAL Patent: JP 2002517507-A 3 18-JUN-2002;
COMMENT MERCK AND CO INC
OS Homo sapiens (human)
PN JP 2002517507-A/3
PD 18-JUN-2002
PF 08-JUN-1999 JP 2000553444
PR 12-JUN-1998 US 60/089098
PI SCOTT D FEIGNER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI
DOUGLAS MACNEIL,
PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH
PC C07K14/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02, PC
C12N15/00
CC Cloning and identification of motilin receptor. FH Key
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FT 1. 1390
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.8e-175;
Matches 1390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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RESULT 4
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DEFINITION Sequence 10310 from Patent WO02068579.
ACCESSION CQ724376
VERSION CQ724376.1 GI:42285233
KEYWORDS Homo sapiens (human)
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ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
Kits, such as nucleic acid arrays, comprising a majority of
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thereof
JOURNAL Patent: WO 02068579-A 10310 06-SEP-2002;
FEATUES PE Corporation (NY) (US)
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Best Local Similarity 89.1%; Pred. No. 7.3e-134;
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;
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Db 61 GCGCTGCGCGCTTGGGACGAGCGCGCTGCTGCGCCCTTTCCCTTGGGGCGCGCTGGTGCGG 120
QY 121 GTGACCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
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QY 181 ATGCTGATCGGGCGCTACCGGGACATCGGGACACACCACTTGTACCTGGGACGATG 240
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QY 1381 GATGGGATAA 1390
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RESULT 5
LOCUS CQ831648 1239 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1 from Patent WO2004057328.
ACCESSION CQ831648
VERSION CQ831648.1 GI:50831561
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Golz,S., Brueggemeier,U. and Summer,H.
TITLE Diagnostics and therapeutics for diseases associated with
JOURNAL g-protein-coupled receptor 38 (gpr38)
Patent: WO 2004057328-A 1 08-JUL-2004;
Bayer HealthCare AG (DE)
FEATURES
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ORIGIN
Query Match 77.6%; Score 1078; DB 6; Length 1239;
Best Local Similarity 89.1%; Pred. No. 7.3e-134;
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;
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RESULT 7
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DEFINITION Sequence 472 from Patent WO02061087.
ACCESSION AX549187
VERSION AX549187.1 GI:25813904
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Burner G.C., Rouh, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 472 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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ORIGIN
Query Match 77.6%; Score 1078; DB 6; Length 1239;
Best Local Similarity 89.1%; Pred. No. 7.3e-134;
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;
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LOCUS
DEFINITION Sequence 1 from Patent WO02057791.

AX572965 1239 bp DNA linear PAT 29-NOV-2002

ACCESSION AX572965
VERSION AX572965.1 GI:26005013
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brown, J.P., Burmer, G.C., Roush, C.L. and Kulander, B.G.
TITLE Diagnostic and therapeutic compositions and methods related to gpr
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JOURNAL Patent: WO 02057791-A 1 25-JUL-2002;
Lifespan Biosciences, Inc. (US)
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DB 1230 GATGGGATAA 1239
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LOCUS 1239 bp mRNA linear PRI 29-MAY-2004
DEFINITION Homo sapiens motilin/ghrelin receptor mRNA, complete cds.
ACCESSION AY603964
VERSION AY603964.1 GI:47571310
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1239)
AUTHORS King, M.M., Aronstam, R.S. and Sharma, S.V.
TITLE Isolation of cDNA coding for motilin/ghrelin receptor (MTLRI/GPR38)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1239)
AUTHORS King, M.M., Aronstam, R.S. and Sharma, S.V.
TITLE Direct Submission
JOURNAL Submitted (20-APR-2004) Guthrie cDNA Resource Center, Guthrie
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ORIGIN		Query Match 77.6%; Score 1078; DB 9; Length 1239;		Best Local Similarity 89.1%; Pred. No. 7.3e-134;		Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;	
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DB	61	GGCTGGCGCTTGGCAGCGCGCTGCTCGCCCTTTCCCTGGGGCGCTGGTGGCG	120	DB	990	GTACTTCTCAGTACTTTAAATCATGCTCGCTCTGCAACTTTTCTATCTGAGCGCATCTAT	104
QY	121	GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180	QY	1201	CAACCCATCTCTACAACTCTTCAAGAGTACAGAGGGGGCGCTTTAACTGCT	126
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DB	181	ATGCTGATCGGCGCTACCGGACATCGGACACCACTGCTGCTGCGGAGCATG	240	DB	1110	GCTCGCAAGGAAGTCCAGGCGGAGAGGCTTCCACAGAGCAGGAGACCTGCGGGGAAGT	116
QY	241	GGCTGTCCGACTACTCATCTGCTGGGCTGCGCTTTCGACTTACCGCTCTGGCGC	300	QY	1321	TGAGGGGACACTGGAGGAGACAGCGTGGGCTACACGAGACAAGCGCTAAAGTGAAGAC	138
DB	241	GGCTGTCCGACTACTCATCTGCTGGGCTGCGCTTTCGACTTACCGCTCTGGCGC	300	DB	1170	TGAGGGGACACTGGAGGAGACAGCGTGGGCTACACGAGACAAGCGCTAAAGTGAAGAC	122
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DB	661	GGGCGGAGACCGGAGCGCGCGCTGTTTACCGCGCGAATGCCGCGGAGCGCGCG	720	AUTHORS	McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D., Hreniuk, D.L., Smith, R.G., Howard, A.D. and Van der Ploeg, L.H.		
QY	721	CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780	TITLE	Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue and neurotensin receptors		
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RESULT 10
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DEFINITION Homo sapiens orphan G protein-coupled receptor (GPR38) gene,
complete cds.
ACCESSION AF034632
VERSION AF034632.1 GI:2654158
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 2040)
AUTHORS McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D.,
Hreniuk, D.L., Smith, R.G., Howard, A.D. and Van der Ploeg, L.H.
Cloning and characterization of two human G protein-coupled
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secretagogue and neurotensin receptors
Genomics 46 (3), 426-434 (1997)
JOURNAL MEDLINE
PUBMED 9441746
REFERENCE 2 (bases 1 to 2040)
AUTHORS McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D.,
Hreniuk, D.L., Smith, R.G., Van Der Ploeg, L.H.T. and Howard, A.D.
Direct Submission
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DEFINITION	Human DNA sequence from clone RP11-203116 on chromosome 13. Contains the gene for KIAA0970 protein, COX7CP1 (cytochrome c oxidase subunit VIIC pseudogene 1), a novel pseudogene, the GPR38 (G protein-coupled receptor 38) gene, ESTs, STSs, GSSs and a CpG island, complete sequence.	
ACCESSION	AL137000.6 GI:9944121	
VERSION	HTG; COX7CP1; CpG island; cytochrome c oxidase; G protein-coupled receptor; GPR38; KIAA0970.	
KEYWORDS	receptor; GPR38; KIAA0970.	
SOURCE	Homo sapiens (human)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 163284)	
AUTHORS	Wall, M.	
TITLE	Direct Submission	
JOURNAL	Submitted (18-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk	
COMMENT	requests: clonerrequest@sanger.ac.uk On Aug 29, 2000 this sequence version replaced gi:9926419. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 IMPORTANT: This sequence is not the entire insert of clone RP11-203116. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.	

The true left end of clone RP11-452110 is at 1 in this sequence.
 The true right end of clone RP11-103018 is at 163284 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-203116 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACE3.6.

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DEFINITION	Homo sapiens chromosome 13 clone Rp11-804, 3 unordered pieces.	
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SOURCE	Homo sapiens (human)	
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REFERENCE		
AUTHORS	Clark, G.	
TITLE	Direct Submission	
JOURNAL	Submitted (08-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk	
COMMENTS	requests: clonerequest@sanger.ac.uk On Aug 10, 2001 this sequence version replaced gi:15131387. ----- Genome Center Center: Sanger Centre Center code: SC Web site: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk ----- Project Information Center project name: BA804 ----- Summary Statistics Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 149716 bases at least Q40 Consensus quality: 150039 bases at least Q30 Consensus quality: 150247 bases at least Q20 Insert size: 341360; sum-of-contigs Insert size: 157238; 2.0% error; agarose-fp Quality coverage: 3.92x in Q20 bases; sum-of-contigs Quality coverage: 8.77x in Q20 bases; agarose-fp	
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QY 961 GCGCAAGCGCTGGGTGCTTCCCTTCCCTGCTGCGCCAGCTCTGGGCGCGCTTCCAGTCCC 1020
DB 320684 GCGCAAGCGCTGGGTGCTTCCCTTCCCTGCTGCGCCAGCTCTGGGCGCGCTTCCAGTCCC 320743
QY 1021 TTTCTATTTCGATTCCAGCTTCCACCGCG 1052
DB 320744 TTTCTATTTCGATTCCAGCTTCCACCGCG 320775

RESULT 13
AX711879 LOCUS 349980 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1 from Patent WO03000727.
ACCESSION AX711879.
VERSION AX711879.1 GI:29787684
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Zhang, Y., Moffatt, M., Cookson, W. and Tinsley, J.O.
AUTHORS Zhang, Y., Moffatt, M., Cookson, W. and Tinsley, J.O.
TITLE Atopy
JOURNAL Patent: WO 03000727-A 1 03-JAN-2003;
ISIS INNOVATION LIMITED (GB)
FEATURES
Location/Qualifiers
source
1..349980
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="Original length of seq 1 to big: 410.846-Splitted
into-seq 1: from 000.001 to 349.980-seq 327: from 300.001
to 410.846-Original length of seq 71 to big:
379.652-Splitted into-seq 71: from 000.001 to 349.980-seq
328: from 300.001 to 379.652"

ORIGIN
Query Match 75.7%; Score 1052; DB 6; Length 349980;
Best Local Similarity 100.0%; Pred. No. 4.8e-131;
Matches 1052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAGCCCTGGAACGGCAGCGCCGCGGGGGCGGGAGCGCGCGTGGCC 60
DB 38016 ATGGCAGCCCTGGAACGGCAGCGCCGCGGGGGCGGGAGCGCGCGTGGCC 38075
QY 61 GCGTGTGCGCTTGGCAGCGCGCTGTCTGCGCTTTTCCCTGGGGCGCTGTGCGG 120
DB 38076 GCGTGTGCGCTTGGCAGCGCGCTGTCTGCGCTTTTCCCTGGGGCGCTGTGCGG 38135
QY 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
DB 38136 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 38195
QY 181 ATGCTGATCGGGCGCTTACCGGAGATCGGACACCACTTGTACTGGGACGATG 240
DB 38196 ATGCTGATCGGGCGCTTACCGGAGATCGGACACCACTTGTACTGGGACGATG 38255
QY 241 GCGGTGTCCGACCTACTCATCTGCTGCGGCTGCGCTTTCGACCTGTACCGCTCTGGGCG 300
DB 38256 GCGGTGTCCGACCTACTCATCTGCTGCGGCTGCGCTTTCGACCTGTACCGCTCTGGGCG 38315
QY 301 TCGGGCCCTGGGTGTGCGGCGCTGTCTGCGGCTGTCTGCGGCTGTCTGCGGCTGTG 360
DB 38316 TCGGGCCCTGGGTGTGCGGCGCTGTCTGCGGCTGTCTGCGGCTGTCTGCGGCTGTG 38375
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Qy 1021 TTTCCTATTTCGATTCCAGCTCCACCGCGG 1052
Db 39036 TTTCCTATTTCGATTCCAGCTCCACCGCGG 39067

RESULT 15
BD211242
LOCUS BD211242 3066 bp DNA linear PAT 17-JUL-2003
DEFINITION Cloning and identification of motilin receptor.
ACCESSION BD211242
VERSION BD211242.1 GI:33021012
KEYWORDS JP 2002517507-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3066)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Feighner, S.D., Patchett, A.A., Tan, C., Mckee, K., Macnei, D.,
Howard, A.D., Pong, S.S. and Smith, R.G.
Cloning and identification of motilin receptor
Patent: JP 2002517507-A 1 18-JUN-2002;
MERCK AND CO INC
COMMENT OS Homo sapiens (human)
PN JP 2002517507-A/1
PD 18-JUN-2002
PF 08-JUN-1999 JP 2000553444
PI 12-JUN-1998 US 60/089098
PI SCOTT D FEIGNER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI
DOUGLAS MACNEIL,
PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH
PC C07K14/705; A61K38/00; A61P1/00; C12N15/09; C12Q1/02; A61K37/02; PC
C12N15/00
CC Cloning and identification of motilin receptor. FH key
Location/Qualifiers
FT source 1..3066
FT /organism="Homo sapiens (human)".
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1..3066
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Best Local Similarity 99.8%; Pred. No. 1.2e-128;
Matches 1050; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Db 1029 ATGGGACGCCCTGTGAACGGGAGCGAGCGGCCCGAGGGGGCGGGAGCGCCCGTGGCCC 1088

Qy 61 GCGGTGCGCGCTTGGGAGCGCGCGTGTCTGCTGCTGGGGGTAGCGGCAACGCTGTGACCGTG 120
Db 1089 GCGGTGCGCGCTTGGGAGCGCGCGTGTCTGCTGCTGGGGGTAGCGGCAACGCTGTGACCGTG 1148

Qy 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
Db 1149 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1208

Qy 181 ATGTGTATCGGGCGCTACCGGGAATCGGGAACACCAACAACTGTGTACCTGGGAGCATG 240
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Qy 241 GCGGTGTCGACCTACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 1269 GCGGTGTCGACCTACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1328

Qy 301 TCGGGCCCTGGGTGTTGGGGCGCGTGTCTGTGCGCCGTGTCCCTCTACGTGGGCGAGGGC 360
Db 1329 TCGGGCCCTGGGTGTTGGGGCGCGTGTCTGTGCGCCGTGTCCCTCTACGTGGGCGAGGGC 1388

Qy 361 TGCACCTACGCCACGCTGTGCATGATGACCGCGCTCAGCGTCTACCTGGCCATC 420
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Search completed: April 11, 2005, 06:41:33
Job time : 6026.47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 11, 2005, 13:13:41 ; Search time 62.3985 Seconds
(without alignments)
3167.746 Million cell updates/sec

Title: US-09-719-485-5
Perfect score: 2043
Sequence: 1 MGSPWNGSDGEGAREBPWP.....WQNHUHKHGRPADVDVLISVL 386

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1581	77.4	412	1 MTLR_HUMAN	O43193 homo sapien
2	674	33.0	295	2 Q6YGZ2	Q6YGZ2 acanthopagr
3	673.5	33.0	363	2 O93413	O93413 spherooides
4	671	32.8	385	2 Q6YGZ3	Q6YGZ3 acanthopagr
5	643	31.5	267	2 Q7ZZJ8	Q7ZZJ8 gallus gall
6	643	31.5	331	2 Q7ZZJ9	Q7ZZJ9 gallus gall
7	643	31.5	366	1 GH5R_HUMAN	Q92847 homo sapien
8	642.5	31.4	360	2 Q6B7N9	Q6B7N9 macaca fasc
9	641.5	31.4	374	2 O93412	O93412 spherooides
10	641	31.4	347	2 Q7ZT14	Q7ZT14 gallus gall
11	641	31.4	364	1 GH5R_MOUSE	O99P50 mus musculu
12	641	31.4	364	1 GH5R_RAT	O08725 rattus norv
13	641	31.4	366	1 GH5R_PIG	Q95254 sus scrofa
14	607	29.7	366	2 Q8MHZ5	Q8MHZ5 ovis aries
15	444	21.7	215	2 Q711Q7	Q711Q7 gallus gall
16	442	21.6	211	2 Q711Q8	Q711Q8 gallus gall
17	435	21.3	559	2 O93414	O93414 spherooides
18	376	18.4	123	2 Q80UB2	Q80UB2 mus musculu
19	356.5	17.4	426	2 Q8NE20	Q8NE20 homo sapien
20	354.5	17.4	403	2 Q7LDP6	Q7LDP6 homo sapien
21	354.5	17.4	426	2 Q9HB85	Q9HB85 homo sapien
22	343	16.8	424	1 NTR1_RAT	P20789 rattus norv
23	340	16.6	424	1 NTR1_MOUSE	O88319 mus musculu
24	339	16.6	145	2 Q97914	Q97914 ovis aries
25	338	16.5	395	2 Q91Z76	Q91Z76 mus musculu
26	338	16.5	395	2 Q8BZ39	Q8BZ39 mus musculu
27	336	16.4	415	2 Q96AM5	Q96AM5 homo sapien
28	335	16.4	412	2 Q7LC54	Q7LC54 homo sapien
29	335	16.4	415	2 Q9GZQ4	Q9GZQ4 homo sapien
30	331.5	16.2	405	2 O55040	O55040 mus musculu
31	330	16.2	418	1 NTR1_HUMAN	P30989 homo sapien

32	329	16.1	395	2 Q9ESQ4	Q9ESQ4 rattus norv
33	329	16.1	395	2 Q9JIB1	Q9JIB1 rattus norv
34	327.5	16.0	493	2 Q7RTK4	Q7RTK4 anopheles g
35	324.5	15.9	309	2 Q7QEG8	Q7QEG8 anopheles g
36	316	15.5	556	1 CAPR_DROME	Q81TC7 drosophila
37	311.5	15.2	413	2 Q65Y5A	Q65Y5A bombyx mori
38	309	15.1	428	2 Q9VFNA	Q9VFNA drosophila
39	309	15.1	430	2 Q8ITC9	Q8ITC9 drosophila
40	308	15.1	453	2 Q7KSK4	Q7KSK4 drosophila
41	308	15.1	295	2 Q7PDF2	Q7PDF2 anopheles g
42	307	15.0	340	2 Q7QBC1	Q7QBC1 anopheles g
43	304.5	14.9	412	2 Q9JJI5	Q9JJI5 rattus norv
44	302.5	14.8	402	2 Q9JIB2	Q9JIB2 rattus norv
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ALIGNMENTS

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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Motilin receptor (G protein-coupled receptor 38).
GN Name=MLNR; Synonyms=GPR38, MTLR, MTLR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=98110578; PubMed=9441746; DOI=10.1006/geno.1997.5069;
RA McKee K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,
RA Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;
RT "Cloning and characterization of two human G protein-coupled receptor
RT genes (GPR38 and GPR39) related to the growth hormone secretagogue and
RT neurotensin receptors.";
RL Genomics 46:426-434 (1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=99316084; PubMed=10381885; DOI=10.1126/science.284.5423.2184;
RA Feighner S.D., Tan C.P., McKee K.K., Palyha O.C., Hreniuk D.L.,
RA Pong S.-S., Austin C.P., Figueroa D., MacNeil D., Cascieri M.A.,
RA Nargund R., Bakshi R., Abramovitz M., Stocco R., Kargman S.,
RA O'Neill G., van Der Ploeg L.H.T., Evans J., Patchett A.A., Smith R.G.,
RA Howard A.D.;
RT "Receptor for motilin identified in the human gastrointestinal
RT system.";
RL Science 284:2184-2188 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=15057823; DOI=10.1038/nature02379;
RA Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,
RA Ashcroft K.J., Beare D.C., Burford D.C., Hunt S.E.,
RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,
RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,
RA Ashwell R.I.S., Babbage A.K., Baggeley C.L., Bailey J., Bannerjee R.,
RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M.,
RA Clegg S.C., Cobley P., Collins J.E., Corby N., Coville G.J.,
RA Deloukas P., Dhali P., Dunham I., Dunn M., Earthrow M.E.,
RA Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,
RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,
RA Grafham D.V., Gribble S.M., Griffiths C., Hall R.E., Hammond S.,
RA Harley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,
RA Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,
RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,
RA Lloyd D.M., Lloyd C., Loveland J.E., Lovell J., Martin S.,
RA Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,

RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
RA Sehra H.K., Showkeen R., Skuce C.D., Smith M., Steward C.A.,
RA Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,
RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
RT "The DNA sequence and analysis of human chromosome 13.",
RL Nature 428:522-528(2004).
RN [4]
RP FUNCTION.
RX MEDLINE=21219832; PubMed=11322507; DOI=10.1385/ENDO.14:1.009;
RA Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D.,
RA Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.,
RT "Growth hormone secretagogue receptor family members and ligands.",
RL Endocrine 14:9-14(2001).
CC -!- FUNCTION: Receptor for motilin.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=O43193-1; Sequences=Displayed;
CC Name=B;
CC IsoId=O43193-2; Sequences=VSP_001894;
CC -!- TISSUE SPECIFICITY: Expressed only in thyroid, stomach, and bone
CC marrow.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF034632; AAC26081.1; -;
CC EMBL; AL137000; CAC19107.1; -;
CC Genew; HGNC:4495; MLNR.
CC MIM; 602885; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
CC GO; GO:0007586; P:digestion; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCR_RHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL_2; 1.
CC KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
CC Transmembrane.
FT DOMAIN 1 35 Extracellular (Potential).
FT TRANSMEM 36 56 1 (Potential).
FT DOMAIN 57 74 Cytoplasmic (Potential).
FT TRANSMEM 75 94 2 (Potential).
FT DOMAIN 95 112 Extracellular (Potential).
FT TRANSMEM 113 134 3 (Potential).
FT DOMAIN 135 157 Cytoplasmic (Potential).
FT TRANSMEM 158 178 4 (Potential).
FT DOMAIN 179 246 Extracellular (Potential).
FT TRANSMEM 247 270 5 (Potential).
FT DOMAIN 271 298 Cytoplasmic (Potential).
FT TRANSMEM 299 320 6 (Potential).
FT DOMAIN 321 334 Extracellular (Potential).
FT TRANSMEM 335 358 7 (Potential).
FT DOMAIN 359 412 Cytoplasmic (Potential).
FT DISULFD 111 235 By similarity.
FT FT N-linked (GlcNAc. . .) (Potential).
FT FT N-linked (GlcNAc. . .) (Potential).
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FT FT QLPYLASINPLNLYNLSKKYRAAFKLLARKSPRGFHR
FT FT SKDTAGEVAGDGGDVGTVGTSTANVKTNG -> RKWSRNG
FT FT SKDACLQSPAPGTAQLGLPLLAQLWAPLPAPFPISIPAS

FT TRCGGGGIYNNLVALPRWQNHLLKHGRFADDDVLSVL
FT (in isoform B).
FT /FTid=VSP_001894.
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Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGSPWNGSDGEGAREPWPALPCDERRCSPFPLGALVPVTAVALCLFVVGVSNNVTV 60
QY 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120
DB 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120
QY 121 CTYATLLHMTALSVERYLAICRPLRVLVTRRRVRLIAVLWAVALLSAGFFFLVGVE 180
DB 121 CTYATLLHMTALSVERYLAICRPLRVLVTRRRVRLIAVLWAVALLSAGFFFLVGVE 180
QY 181 QDRGISVVGNGTARTASSPLASPLWLSRAPPSPSPETAARAALESRCRPSPA 240
DB 181 QDRGISVVGNGTARTASSPLASPLWLSRAPPSPSPETAARAALESRCRPSPA 240
QY 241 QLGLRVLVMTVTTAYFFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGRHRTVRL 300
DB 241 QLGLRVLVMTVTTAYFFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGRHRTVRL 300
RESULT 2
Q6VYZ2 PRELIMINARY; PRT; 295 AA.
ID Q6VYZ2
AC Q6VYZ2
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Growth hormone secretagogue receptor 1b.
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI TaxID=72011;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15062547; DOI=10.1016/j.mce.2003.11.020;
RA Chan C.B., Cheng C.H.K.;
RT "Identification and functional characterization of two alternatively
RT spliced growth hormone secretagogue receptor transcripts from the
RT pituitary of black seabream Acanthopagrus schlegelii.",
RL Mol. Cell. Endocrinol. 214:81-95(2004).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC EMBL; AY151041; AAN7876.1; -;
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
CC InterPro; IPR003905; GHSI_receptor.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR01417; GHSRECEPTOR.
CC PRINTS; PR00237; GPCR_RHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL_2; 1.
CC KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 295 AA; 33883 MW; E7397DCABDF73873 CRC64;
Query Match 33.0%; Score 674; DB 2; Length 295;
Best Local Similarity 45.3%; Pred. No. 3.9e-38;
Matches 141; Conservative 43; Mismatches 73; Indels 54; Gaps 7;


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QY 17 PPWALPPCDERRCS-----PPPLG-----ALVPVTAVCLCFVVGSGNV 57
Db 2 PSWPNLSECLSNCSWEETRNRATKFDLGLPLNTYISPLLTGTITACTLLFLVGVAGNV 61
QY 58 VTMVLIQYRDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYV 117
Db 62 MTLVWSKYRDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYV 121
QY 118 GEGCTYATLLHMTALSVRYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLV 177
Db 122 SESCTYSILSITALSVRYLAICRPLAKALVTRRRVRALIAVLWAVALLSAGPFLFLV 181
QY 178 GVEOD---PGISVPLNGTARIASSPLASSPPLWLSRAPPSPPSGPETAFAALFSRE 234
Db 182 GVERDSMPGNLSWVGNGTGF-----PEEGD-----TRE 212
QY 235 CPSP--PAQLGNLRVLMVNTTAYFPLPFLCLSLILYGLIGRELWSSRPRLR-GPAASGRER 291
Db 213 CMNTHYAVESGLMGAMVLLSSVFFPMPVCLTVLYSLIGRLLWQRHRETNINSRVAREK 272
QY 292 GHROTVRVLK 302
Db 273 SNRQIKMLGK 283

RESULT 3
O93413
ID O93413 PRELIMINARY; PRT; 363 AA.
AC O93413;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Orphan G protein-coupled receptor.
OS Spherozooids nephelus
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Spherozooids.
OX NCBI_TaxID=39110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20922336; PubMed=1628755; DOI=10.1210/me.14.1.160;
RA Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hreniuk D.L.,
RA Gao Y.D., Schleim K.D., Yang L., Mortiello G.J., Nargund R.,
RA Patchett A.A., Howard A.D., Smith R.G.;
RT "Ligand activation domain of human orphan growth hormone (GH)
secretagogue receptor (GHS-R) conserved from Pufferfish to humans.";
RL Mol. Endocrinol. 14:160-169(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF082210; AAC33473.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GH51 receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GH5RECEPTOR.
DR PROSITE; PS00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 363 AA; 41324 MW; 74518BD9CD310991 CRC64;

Query Match 33.0%; Score 673.5; DB 2; Length 363;
Best Local Similarity 49.6%; Pred. No. 5.2e-38;
Matches 135; Conservative 39; Mismatches 55; Indels 43; Gaps 4;

QY 31 SPFGALVPVAVCLCFVVGSGNVVTVMLIGRYRDMRTTNNLYLGSMAVSDLLILGL 90

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Db 31 SLFPASTLIPVTVICILIFVVGVTGNTWTILLIQFKDMKTTNNLYLSSMAVSDLVIFLC 90
QY 91 LPFDLYRLWRSRPWVFGPLLCRLSLYVGEGETYATLLHMTALSVRYLAICRPLRARVLV 150
Db 91 LPFDLYRLWRSRPWVFGPLLCRLSLYVGEGETYATLLHMTALSVRYLAICRPLRARVLV 150
QY 151 TRRRVRALIAVLWAVALLSAGPFLFLVGVGEQDPGISVVGPLNGTARIASSPLASSPPLW 210
Db 151 TRRRVRALIAVLWAVALLSAGPFLFLVGVGEQDPGISVVGPLNGTARIASSPLASSPPLW 210
QY 211 SRAPPPSPSGPETAFAALFSRRCRPSAOL--GALRVMLVNTTAYFPLPFLCLSLYV 268
Db 186 ----HPDNTG-----QCKHTGYAISGQLHIMLVWSTTYFFCPMLCLFLYV 229
QY 269 LIGRELWSSRPRLRGPASGRGRHROTVRVL 300
Db 230 SIGCKLWKSNDLQPCALARESHROTIVKIL 261

RESULT 4
Q6YGZ3
ID Q6YGZ3 PRELIMINARY; PRT; 385 AA.
AC Q6YGZ3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Growth hormone secretagogue receptor 1a.
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI_TaxID=72011;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1562547; DOI=10.1016/j.mce.2003.11.020;
RA Chan C.B., Cheng C.H.K.;
RT "Identification and functional characterization of two alternatively
spliced growth hormone secretagogue receptor transcripts from the
pituitary of black seabream Acanthopagrus schlegelii.";
RL Mol. Cell. Endocrinol. 214:81-95(2004).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY151040; AAN7875.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GH51 receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GH5RECEPTOR.
DR PROSITE; PS00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 385 AA; 43697 MW; 665CBDA9702887A9 CRC64;

Query Match 32.8%; Score 671; DB 2; Length 385;
Best Local Similarity 45.3%; Pred. No. 8.1e-38;
Matches 140; Conservative 43; Mismatches 72; Indels 54; Gaps 7;

QY 17 PPWALPPCDERRCS-----PPPLG-----ALVPVTAVCLCFVVGSGNV 57
Db 2 PSWPNLSECLSNCSWEETRNRATKFDLGLPLNTYISPLLTGTITACTLLFLVGVAGNV 61
QY 58 VTMVLIQYRDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYV 117
Db 62 MTLVWSKYRDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYV 121
QY 118 GEGCTYATLLHMTALSVRYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLV 177

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Db 122 SESCTYSTILSTALSVRYLAICPPLAKALVTKRRVRLALLLWTVSLLSAGPVFMV 181
QY 178 GVEQD---PGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALPSRE 234
Db 182 GVERDSWPNGLSWGNGTGFF-----PEEGD-----TRE 212
QY 235 CPSP--PAQLGALRVMLVNTAYFELPFLCLSLYGLIGRELWSSRRPLR-GPAASGRER 291
Db 213 CKNTHYAVESGLGAMVWLLSVFFPMPVFCULTVLYSLIGRLWQRHRETNINSRVAREK 272
QY 292 GHRQTVRVL 300
Db 273 SNRQIKML 281

RESULT 5
Q7ZZJ8 PRELIMINARY; PRT; 267 AA.
AC Q7ZZJ8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type 1b.
GN Name=Ghar1b;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Pituitary;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Wakita M., Shimada K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB095997; BAC76446.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GPCR_Rhodopsin.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 267 AA; 30209 MW; 00563690B35AD107 CRC64;

Query Match 31.5%; Score 643; DB 2; Length 267;
Best Local Similarity 44.4%; Pred. No. 4.6e-36;
Matches 126; Conservative 54; Mismatches 56; Indels 48; Gaps 5;

QY 33 PPLGALVPVAVCLCLFVVGSGNVVTVMLIGRYDRMTTNLYLGSMAVSDLLILGLP 92
Db 19 FPAPVLGTITVACVLLFVVGVLGNLMTLVVSRFRDMRTTNLYLSSMAFSDLLILFLCP 78
QY 93 FDLVRLWRSRPVFGPFLCLRLSLYVGECGTATLLHMTALSVERYLAI CRPLARVLVTR 152
Db 79 LDFRLWQYRPWNFGDLCKLKFQFISECTYSTILNITALSVRYVAICFPLRAKVIITK 138
QY 153 RYRVALIAMLAVALLSAGPFLFLVGVEODPGISVVPGLNGTARIASSPLASSPPLWLSR 212
Db 139 RKVKLVILLWAVSFISAGPIFLVGVGHE-----NGT-----NPLSTN----- 177
QY 213 APPSPSPGPTAEAAALFSRECRPSAQL--GALRVMLWVTYATYFPLFCILSILYGLI 270
Db 178 -----ECRATEYAIRSGLLTIMWISSIFFFLPVFCLTVLSLI 216
QY 271 GRELWSSRRPLRGPAAASGRGRHQTQTVRLRKWSKDACLIQ 314

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Db 217 GRKLWRRKRNIGSTTIIRKNNKQTVKLMGAPRA-----LCLQ 256

RESULT 6
Q7ZZJ9 PRELIMINARY; PRT; 331 AA.
AC Q7ZZJ9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type la variant.
GN Name=Ghar1av;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Pituitary;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Ohta Y., Tsushima N.,
RA Wakita M., Shimada K.;
RT "Molecular characterization of chicken growth hormone secretagogue
receptor gene."
RL Gen. Comp. Endocrinol. 134:198-202(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB095996; BAC76445.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GPCR_Rhodopsin.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 331 AA; 37567 MW; 1BE477BF2D7A3BEB CRC64;

Query Match 31.5%; Score 643; DB 2; Length 331;
Best Local Similarity 44.7%; Pred. No. 5.6e-36;
Matches 122; Conservative 56; Mismatches 51; Indels 44; Gaps 4;

QY 33 PPLGALVPVAVCLCLFVVGSGNVVTVMLIGRYDRMTTNLYLGSMAVSDLLILGLP 92
Db 19 FPAPVLGTITVACVLLFVVGVLGNLMTLVVSRFRDMRTTNLYLSSMAFSDLLILFLCP 78
QY 93 FDLVRLWRSRPVFGPFLCLRLSLYVGECGTATLLHMTALSVERYLAI CRPLARVLVTR 152
Db 79 LDFRLWQYRPWNFGDLCKLKFQFISECTYSTILNITALSVRYVAICFPLRAKVIITK 138
QY 153 RYRVALIAMLAVALLSAGPFLFLVGVEODPGISVVPGLNGTARIASSPLASSPPLWLSR 212
Db 139 RKVKLVILLWAVSFISAGPIFLVGVGHE-----NGT-----NPLSTN----- 177
QY 213 APPSPSPGPTAEAAALFSRECRPSAQL--GALRVMLWVTYATYFPLFCILSILYGLI 270
Db 178 -----ECRATEYAIRSGLLTIMWISSIFFFLPVFCLTVLSLI 216
QY 271 GRELWSSRRPLRGPAAASGRGRHQTQTVRLRKW 303
Db 217 GRKLWRRKRNIGSTTIIRKNNKQTVKLMGRY 249

RESULT 7
GHSR_HUMAN
ID GHSR_HUMAN STANDARD; PRT; 366 AA.

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OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=kidney, and Pituitary;
RX MEDLINE=22874039; PubMed=14511992; DOI=10.1016/S0016-6480(03)00247-8;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Ohta Y., Tsushima N.,
RA Wakita M., Shimada K.;
RT "Molecular characterization of chicken growth hormone secretagogue
receptor gene."
RL Gen. Comp. Endocrinol. 134:198-202(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB095994; BAC76443.1; -
DR EMBL; AB095995; BAC76444.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GHSI_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_HODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 347 AA; 39439 MW; 7A7543A9A94222F4 CRC64;

Query Match 31.4%; Score 641; DB 2; Length 347;
Best Local Similarity 45.2%; Pred. No. 8.1e-36;
Matches 122; Conservative 54; Mismatches 50; Indels 44; Gaps 4;

QY 33 PFLGALVPVAVCLCLFVVGSGNVVTVMLIGRYDRMTTNLYLGSMVAGDILLILGLP 92
DB 19 FPAPVLTGTVACVLLFVVGVLGNLTMLVSVRFDRMTTNLYLSSMAFSDLLIFLCMP 78

QY 93 FDLVRLWRSRPMVFGPLCRISLYVGECTYATLLHMTALSVERYLAICRLRVLVTR 152
DB 79 LDLPLWQVRFVWFGDLCKLFQFISECTYSTILNITALSVERYVAICFLRAKVIITK 138

QY 153 RVRVALIAVWALLSAGPLFLVGVQDQGISVVGNGTARTASSPLASSPPLWLSR 212
DB 139 RKVLLVILWAVSFISAPFVLGVGEH-----NGT-----NPLSTN----- 177

QY 213 APPSPSPGPETAFAALFSRECRPSAQL--GALRVMLWVTVTFYFFLPCLSLYGLI 270
DB 178 -----ECRATEYAIRSGLLTIWNISSIFFFLPFLVCLIVLYSLI 216

QY 271 GRELWSSRRPLRGPAASGRGRHQTQVRL 300
DB 217 GRKLWRRKKNIGPSTIIRDKNNKQTVKWL 246

RESULT 11
GHSR MOUSE
ID GHSR MOUSE STANDARD; PRT; 364 AA.
AC Q99F50; QBWXB; Q91282;
DT 28-FEB-2003 (Rel. 41, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
DE peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=Ghar;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=22354683; PubMed=12466951; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

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RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gastermond S., Gutinchin S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawagawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Nagashima T., Numata K., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Marchionni L., McKenzie L., Miki H.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelain A., Schneider C., Semple C.A., Setou M., Shimada M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RN Nature 420:563-573(2002).
RL [2]
RP SEQUENCE OF 1-183 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RA Kacsob B.;
RT "Cloning of mouse ghrelin/growth hormone secretagogue receptor cDNA by
RT rapid amplification of cDNA ends (RACE)."
RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE OF 73-257 FROM N.A.
RC STRAIN=129S3/SvimJ;
RA Peng X., Frohman L.A., Kineman R.D.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth
CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692,429, MK-0677, adenosine) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AK049671; BAC33866.1; -
CC EMBL; AY056474; AAL13336.1; -
CC EMBL; AF332997; AAG61141.1; -
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCR_HODOPSIN.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Transmembrane.
KW DOMAIN 1 40 Extracellular (Potential).
FT TRANSMEM 41 66 1 (Potential).
FT DOMAIN 67 72 Cytoplasmic (Potential).
FT TRANSMEM 73 96 2 (Potential).
FT DOMAIN 97 117 Extracellular (Potential).
FT TRANSMEM 118 139 3 (Potential).
FT DOMAIN 140 162 Cytoplasmic (Potential).
FT TRANSMEM 163 183 4 (Potential).

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FT DOMAIN 184 211 Extracellular (Potential).
FT TRANSMEM 212 235 5 (Potential).
FT DOMAIN 236 263 Cytoplasmic (Potential).
FT TRANSMEM 264 285 6 (Potential).
FT DOMAIN 286 302 Extracellular (Potential).
FT TRANSMEM 303 326 7 (Potential).
FT DOMAIN 327 364 Cytoplasmic (Potential).
FT DISULFID 115 197 By similarity.
FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 187 187 N-linked (GlcNAc...) (Potential).
FT CONFLICT 59 59 G -> S (in Ref. 2).
SQ SEQUENCE 364 AA; 40963 MW; 8F1214E585F3B2E8 CRC64;

Query Match 31.4%; Score 641; DB 1; Length 364;
Best Local Similarity 45.8%; Pred. No. 8.5e-36;
Matches 142; Conservative 41; Mismatches 65; Indels 62; Gaps 10;

QY 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPFLGALVPTAVCLCLFVVGSG 55
Db 2 WNAT--PSEPEPNVTLDDWDASGNDLSDELPLFPAPLAGVATATCVAFVVGISG 59

QY 56 NVVTMLIGRYDMRTTNLYLGMAVSDLLILGLPDLVRLMRSRPWFGLLCRLSL 115
Db 60 NLLTMLVSRFRRLRTTNLYLSSMAFSDLLIFLCPLDLVRLMQRPNFGLDLCKLFQ 119

QY 116 YVGECTYATLHMTALSVERYLACRPLRARVLTTRRVRALIAVLAVALLSAGPFLF 175
Db 120 FVSECTYATVLTITALSVERYFAICFLRAKVVTKGRVKLVILVAVAFCSAGPFLV 179

QY 176 LVGVQDQGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAAALFSREC 235
Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197

QY 236 RPS--PAQIGALRVLMTVTFVFPFLCLSLYLIGRELWSSRRPLRGPASG---RE 290
Db 198 RATEFAVRSGLLTVMVSVSFFFLVFLVCLTVLSLIGRLW--RR--RGDAAVGSLRD 253

QY 291 RGHRTQTVRL 300
Db 254 QNHQTQVKML 263

RESULT 12
GHSR_RAT
ID GHSR_RAT STANDARD; PRT; 364 AA.
AC O08725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
DE peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=Ghsr;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=97246555; PubMed=9092793; DOI=10.1210/me.11.4.415;
RA McKee K.K., Palyha O.C., Feighner S.D., Hreniuk D.L., Tan C.P.,
RA Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.;
RT "Molecular analysis of rat pituitary and hypothalamic growth hormone
RT secretagogue receptors.";
RL Mol. Endocrinol. 11:415-423 (1997).
RN [2]
RP SEQUENCE OF 1-240 FROM N.A.
RC STRAIN=Wistar; TISSUE=Pituitary;
RX MEDLINE=98100386; PubMed=9437712; DOI=10.1016/S0196-9781(97)00263-5;
RA Yokote R., Sato M., Matsubara S., Ohye H., Niimi M., Murao K.,
RA Takahara J.;
RT "Molecular cloning and gene expression of growth hormone-releasing

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peptide receptor in rat tissues.";
Peptides 19:15-20 (1998).
[3]
RP FUNCTION.
RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from
RT stomach.";
RL Nature 402:656-660 (1999).
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth
CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692,429, MK-0677, adenosine) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U94321; AAC53156.1; -.
CC EMBL; AB001982; BAA31777.1; ALT_INIT.
CC RGD; 621397; Ghsr.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Transmembrane.
CC DOMAIN 1 40 Extracellular (Potential).
FT TRANSMEM 41 66 1 (Potential).
FT DOMAIN 67 72 Cytoplasmic (Potential).
FT TRANSMEM 73 96 2 (Potential).
FT DOMAIN 97 117 Extracellular (Potential).
FT TRANSMEM 118 139 3 (Potential).
FT DOMAIN 140 162 Cytoplasmic (Potential).
FT TRANSMEM 163 183 4 (Potential).
FT DOMAIN 184 211 Extracellular (Potential).
FT TRANSMEM 212 235 5 (Potential).
FT DOMAIN 236 263 Cytoplasmic (Potential).
FT TRANSMEM 264 285 6 (Potential).
FT DOMAIN 286 302 Extracellular (Potential).
FT TRANSMEM 303 326 7 (Potential).
FT DOMAIN 327 364 Cytoplasmic (Potential).
FT DISULFID 115 197 By similarity.
FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 187 187 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 364 AA; 40963 MW; DCBF559B8061EE9 CRC64;

Query Match 31.4%; Score 641; DB 1; Length 364;
Best Local Similarity 45.8%; Pred. No. 8.5e-36;
Matches 142; Conservative 41; Mismatches 65; Indels 62; Gaps 10;

QY 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPFLGALVPTAVCLCLFVVGSG 55
Db 2 WNAT--PSEPEPNVTLDDWDASGNDLSDELPLFPAPLAGVATATCVAFVVGISG 59

QY 56 NVVTMLIGRYDMRTTNLYLGMAVSDLLILGLPDLVRLMRSRPWFGLLCRLSL 115
Db 60 NLLTMLVSRFRRLRTTNLYLSSMAFSDLLIFLCPLDLVRLMQRPNFGLDLCKLFQ 119

QY 116 YVGECTYATLHMTALSVERYLACRPLRARVLTTRRVRALIAVLAVALLSAGPFLF 175
Db 120 FVSECTYATVLTITALSVERYFAICFLRAKVVTKGRVKLVILVAVAFCSAGPFLV 179

QY 176 LVGVQDQGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAAALFSREC 235
Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197

QY 236 RPS--PAQIGALRVLMTVTFVFPFLCLSLYLIGRELWSSRRPLRGPASG---RE 290
Db 198 RATEFAVRSGLLTVMVSVSFFFLVFLVCLTVLSLIGRLW--RR--RGDAAVGSLRD 253

QY 291 RGHRTQTVRL 300
Db 254 QNHQTQVKML 263

RESULT 12
GHSR_RAT
ID GHSR_RAT STANDARD; PRT; 364 AA.
AC O08725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
DE peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=Ghsr;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=97246555; PubMed=9092793; DOI=10.1210/me.11.4.415;
RA McKee K.K., Palyha O.C., Feighner S.D., Hreniuk D.L., Tan C.P.,
RA Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.;
RT "Molecular analysis of rat pituitary and hypothalamic growth hormone
RT secretagogue receptors.";
RL Mol. Endocrinol. 11:415-423 (1997).
RN [2]
RP SEQUENCE OF 1-240 FROM N.A.
RC STRAIN=Wistar; TISSUE=Pituitary;
RX MEDLINE=98100386; PubMed=9437712; DOI=10.1016/S0196-9781(97)00263-5;
RA Yokote R., Sato M., Matsubara S., Ohye H., Niimi M., Murao K.,
RA Takahara J.;
RT "Molecular cloning and gene expression of growth hormone-releasing

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Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197

Qy 236 RPS--PAQIGALRVMLWVTYFFLPFLCLSLYGLIGRELWSSRRPLRGPASG---RE 290

Db 198 RATEFAVRSGLLTVMVWSSVFFFLPVFCLTLVLYSLIGRKLW--RR--RGDAVAGSLRD 253

Qy 291 RGHRTQVRVL 300

Db 254 QNHQTVKML 263

RESULT 13

GHSR_PIG STANDARD; PRT; 366 AA.

AC Q95254; Q95255;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing peptide receptor) (GHRP) (Ghrelin receptor).

GN Name=GHSR;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).

RX MEDLINE=96337998; PubMed=8668086;

RA Howard A.D., Feighner S.D., Cully D.F., Arena J.P., Liberators P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L., Palya O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu K.K., McKee K.K., Pong S.-S., Chung L.-Y., Elbrecht A., Dashkevich M., Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G., Patchett A.A., Narund R., Griffin P.R., Demartino J.A., Gupta S.K., Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.;

RT "A receptor in pituitary and hypothalamus that functions in growth hormone release."

RL Science 273:974-977 (1996).

CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins. Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6) as well as non-peptide, low molecular weight secretagogues (e.g. L-692,429, MK-0677, adenosine).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=1A;

CC IsoID=Q95254-1; Sequence=Displayed;

CC Name=1B;

CC IsoID=Q95254-2; Sequence=VSP 001918, VSP 001919;

CC -!- TISSUE SPECIFICITY: Pituitary and hypothalamus.

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; U60178; AAC48630.1; -

DR EMBL; U60180; AAC48631.1; -

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm1.1; 1.

DR PRINTS; PR00237; GPCRHHODOPSIN.

DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; 1.

DR PROSITE; PS00262; G PROTEIN RECEPTOR F1.2; 1.

KW Alternative splicing; G-protein coupled receptor; Glycoprotein; Transmembrane.

FT DOMAIN 1 40 Extracellular (Potential).

FT TRANSMEM 41 66 1 (Potential).

FT DOMAIN 67 72 Cytoplasmic (Potential).

FT TRANSMEM 73 96 2 (Potential).

FT DOMAIN 97 117 Extracellular (Potential).

FT TRANSMEM 118 139 3 (Potential).

FT DOMAIN 140 162 Cytoplasmic (Potential).

FT TRANSMEM 163 183 4 (Potential).

FT DOMAIN 184 211 Extracellular (Potential).

FT TRANSMEM 212 235 5 (Potential).

FT DOMAIN 236 263 Cytoplasmic (Potential).

FT TRANSMEM 264 285 6 (Potential).

FT DOMAIN 286 302 Extracellular (Potential).

FT TRANSMEM 303 326 7 (Potential).

FT DOMAIN 327 366 Cytoplasmic (Potential).

FT DISULFID 116 198 By similarity.

FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 27 27 N-linked (GlcNAc...) (Potential).

FT VARSPLIC 266 289 AVVVFAPILCVLPFHVGRVLFPSKS -> GGSQALELSLPG

FT PLHSSCLFSSP (in isoform 1B).

FT FTID=VSP 001918.

FT Missing (in isoform 1B).

FT FTID=VSP 001919.

FT VARSPLIC 290 366

FT SEQUENCE 366 AA; 41194 MW; 2C850B3EF61B7C1C CRC64;

Qy 5 WNGSDPEGA-----REPPWALPCD---ERRCSPPFLGALVPVAVCLCLFVVGVSGN 56

Db 2 WNAPESEPGNLTLPDLGWDPENDSLVELLPFTPLLAGVTATCVLFVVGIA 61

Qy 57 VVTVMILGRYDRMTTNYLIGSMVSDLLILLGLFDLYRLWRRPWPVFGPLCLRLSLY 116

Db 62 LLTVMVSRFRMTTNYLSSMAFSLILFLCPLDLFRLWQYRPWNLGKLLKLFQF 121

Qy 117 VEGCTATLHMTALSVERYLAICRPLARAVVTRRVRALIAVLWAVALLSAGPFLFL 176

Db 122 VSECTATVITLITALSVERYFAICFPURAKVVVTKGRVKLVILWAVAFCSAGPIFVL 181

Qy 177 VGEVDQPGISVVPGLNGTARIASSPLASSPPLWLRAPPPSPPPSGPETAFAALFSRECR 236

Db 182 VGVEHD-----NGT-----DPRD-----TNECR 199

Qy 237 PS--PAQIGALRVMLWVTYFFLPFLCLSLYGLIGRELWSSRRPLRGPASG---RER 291

Db 200 ATEFAVRSGLLTVMVWSSVFFFLPVFCLTLVLYSLIGRKLW---RRKGEAAVGSLSRDQ 256

Qy 292 GHRQTVRVL 300

Db 257 NHHQTVKML 265

RESULT 14

QBMHZ5 QBMHZ5 PRELIMINARY; PRT; 366 AA.

AC Q8MHZ5;

DT 01-OCT-2002 (TREMELrel. 22, Created)

DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)

DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)

DE Ghrelin/growth hormone secretagogue receptor.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Pituitary gland;

RA Murata T., Ikegami R., Morita Y., Shinozaki K.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

DR EMBL; AY093948; AAM19733.1; -

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:51:55 ; Search time 503.911 Seconds
(without alignments)
9955.765 Million cell updates/sec

Title: US-09-719-485-1
Perfect score: 3066
Sequence: 1 ttgaattatctgtcactg.....acgtgaacatgggataa 3066

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTBUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	9.2	283	US-08-993-088A-4	Sequence 4, Appli
2	283	9.2	283	US-08-993-424B-4	Sequence 4, Appli
3	283	9.2	283	US-09-603-680-4	Sequence 4, Appli
4	248.2	8.1	1050	US-09-762-661A-1	Sequence 1, Appli
5	234.8	7.7	1063	US-09-077-675A-1	Sequence 1, Appli
6	234.8	7.7	1063	US-09-077-674-1	Sequence 1, Appli
7	231.6	7.6	1095	US-09-743-475-2	Sequence 2, Appli
8	231.6	7.6	4009	US-09-743-475-1	Sequence 1, Appli
9	230	7.5	1029	US-09-077-675A-4	Sequence 4, Appli
10	230	7.5	1029	US-09-077-674-4	Sequence 4, Appli
11	229	7.5	250	US-09-016-434-359	Sequence 359, App
12	228.8	7.5	1122	US-09-077-675A-9	Sequence 9, Appli
13	228.8	7.5	1122	US-09-077-674-9	Sequence 15, Appli
14	228.4	7.4	1092	US-09-077-674-15	Sequence 15, Appli
15	228.4	7.4	1092	US-09-077-675A-14	Sequence 14, Appli
16	228.4	7.4	3129	US-09-077-674-14	Sequence 14, Appli
17	228.4	7.4	3129	US-09-077-675A-6	Sequence 6, Appli
18	227.8	7.4	1088	US-09-077-675A-6	Sequence 6, Appli
19	227.8	7.4	1088	US-09-077-674-6	Sequence 6, Appli
20	227.8	7.4	1101	US-09-016-434-1148	Sequence 1148, Ap
21	227.8	7.4	1101	US-09-170-496D-87	Sequence 87, Appli
22	227.8	7.4	1101	US-09-170-496D-209	Sequence 209, App
23	227.8	7.4	1101	US-09-364-425B-44	Sequence 44, Appli
24	206.8	6.7	37004	US-09-949-016-15317	Sequence 15317, A
25	202.2	6.6	29629	US-09-729-995-3	Sequence 3, Appli
26	202.2	6.6	29629	US-10-135-689-3	Sequence 3, Appli
27	202.2	6.6	29629	US-10-690-617-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-993-088A-4
Sequence 4, Application US/08993088A
Patent No. 6287855

GENERAL INFORMATION:

APPLICANT: Tan, Carina
APPLICANT: Sullivan, Kathleen
TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,088A

FILING DATE: 18-DEC-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/033,851

FILING DATE: 27-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 19846

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-1958

TELEFAX: 732-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 283 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Other

LOCATION: 1...283

OTHER INFORMATION: cdna probe

US-08-993-088A-4

Sequence 16038, A
Sequence 165371,
Sequence 16402, A
Sequence 15870, A
Sequence 165372,
Sequence 165373,
Sequence 13555, A
Sequence 77323, A
Sequence 14000, A
Sequence 12517, A
Sequence 16021, A
Sequence 14577, A
Sequence 14578, A
Sequence 77324, A
Sequence 12683, A
Sequence 13194, A
Sequence 77322, A
Sequence 13220, A

Query Match 9.2%; Score 283; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.3e-49;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1234 TGGGACACCAACAACTTGTACCTGGGAGCATGGCGGTTCGACCTACTCATCTGTC 1293
DB 1 TGGGACACCAACCAACAACTTGTACCTGGGAGCATGGCGGTTCGACCTACTCATCTGTC 60
QY 1294 TGGGCTGCGGCTTCGACCTGTACCGCTCTGGCGCTTCGCGCCCTGGGTGTTCGGGCGC 1353
DB 61 TGGGCTGCGGCTTCGACCTGTACCGCTCTGGCGCTTCGCGCCCTGGGTGTTCGGGCGC 120
QY 1354 TGCTCTGCGGCTTCGACCTGTACCGCTTCGCGAGGCTGCACCTAGCCACGCTGTGTGACA 1413
DB 121 TGCTCTGCGGCTTCGACCTGTACCGCTTCGCGAGGCTGCACCTAGCCACGCTGTGTGACA 180
QY 1414 TGACCGCGCTCAGCGTTCGAGCGCTACCTGGGCATCTGCCGCCGCTTCGCGCCCGCTCT 1473
DB 181 TGACCGCGCTCAGCGTTCGAGCGCTACCTGGGCATCTGCCGCCGCTTCGCGCCCGCTCT 240
QY 1474 TGGTACCGCGCGCGCTTCGCGCGCTCATCGCTGTGCTCTG 1516
DB 241 TGGTACCGCGCGCGCTTCGCGCGCTCATCGCTGTGCTCTG 283

RESULT 2

US-08-993-424B-4
; Sequence 4, Application US/08993424B
; Patent No. 6337206
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Kolakowski, Lee F., Jr.
; TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALR2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,424B
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846NP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...283
; OTHER INFORMATION: cDNA probe

US-08-993-424B-4

Query Match 9.2%; Score 283; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.3e-49;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1234 TGGGACACCAACAACTTGTACCTGGGAGCATGGCGGTTCGACCTACTCATCTGTC 1293
DB 1 TGGGACACCAACCAACAACTTGTACCTGGGAGCATGGCGGTTCGACCTACTCATCTGTC 60
QY 1294 TGGGCTGCGGCTTCGACCTGTACCGCTCTGGCGCTTCGCGCCCTGGGTGTTCGGGCGC 1353
DB 61 TGGGCTGCGGCTTCGACCTGTACCGCTCTGGCGCTTCGCGCCCTGGGTGTTCGGGCGC 120
QY 1354 TGCTCTGCGGCTTCGACCTGTACCGCTTCGCGAGGCTGCACCTAGCCACGCTGTGTGACA 1413
DB 121 TGCTCTGCGGCTTCGACCTGTACCGCTTCGCGAGGCTGCACCTAGCCACGCTGTGTGACA 180
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DB 181 TGACCGCGCTCAGCGTTCGAGCGCTACCTGGGCATCTGCCGCCGCTTCGCGCCCGCTCT 240
QY 1474 TGGTACCGCGCGCGCTTCGCGCGCTCATCGCTGTGCTCTG 1516
DB 241 TGGTACCGCGCGCGCTTCGCGCGCTCATCGCTGTGCTCTG 283

RESULT 3

US-09-603-680-4
; Sequence 4, Application US/09603680
; Patent No. 6544753
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Sullivan, Kathleen
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/603,680
; FILING DATE: 26-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; APPLICATION NUMBER: 08/993,088
; FILING DATE: 18-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846 CA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other


```

1 Patent No. 6500938
2 /
3 GENERAL INFORMATION:
4 /
5 APPLICANT: Janice Au-Young
6 /
7 APPLICANT: Jeffrey J. Seilhamer
8 /
9 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
10 /
11 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
12 /
13 NUMBER OF SEQUENCES: 1490
14 /
15 CORRESPONDENCE ADDRESS:
16 /
17 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
18 /
19 STREET: 3174 PORTER DRIVE
20 /
21 CITY: PALO ALTO
22 /
23 STATE: CALIFORNIA
24 /
25 COUNTRY: USA
26 /
27 ZIP: 94304
28 /
29 COMPUTER READABLE FORM:
30 /
31 MEDIUM TYPE: Floppy disk
32 /
33 COMPUTER: IBM PC compatible
34 /
35 OPERATING SYSTEM: PC-DOS/MS-DOS
36 /
37 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
38 /
39 CURRENT APPLICATION DATA:
40 /
41 APPLICATION NUMBER: US/09/016,434
42 /
43 FILING DATE: HEREMITH
44 /
45 CLASSIFICATION:
46 /
47 PRIOR APPLICATION DATA:
48 /
49 APPLICATION NUMBER:
50 /
51 FILING DATE:
52 /
53 CLASSIFICATION:
54 /
55 ATTORNEY/AGENT INFORMATION:
56 /
57 NAME: Zeller, Karen J.
58 /
59 REGISTRATION NUMBER: 37,071
60 /
61 REFERENCE/DOCKET NUMBER: PA-0002 US
62 /
63 TELECOMMUNICATION INFORMATION:
64 /
65 TELEPHONE: (650) 855-0555
66 /
67 TELEFAX: (650) 845-4166
68 /
69 INFORMATION FOR SEQ ID NO: 359:
70 /
71 SEQUENCE CHARACTERISTICS:
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73 LENGTH: 250 base pairs
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75 TYPE: nucleic acid
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77 STRANDEDNESS: single
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79 TOPOLOGY: linear
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81 IMMEDIATE SOURCE:
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83 LIBRARY: TFPINOT01
84 /
85 CLONE: 2018536
86 /
87 US-09-016-434-359

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Qy	2884	ATCCTCTACAACCTCATTTCAAAGAGTACAGAGCGCGCGCTTTAAACTGCTGCTCGCA	2943	
Db	61	ATCCTCTACAACCTCATTTCAAAGAGTACAGAGCGCGCGCTTTAAACTGCTGCTCGCA	120	
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Qy	3004	GACACTGGAGGAGACACGGTGGGCTACACCGAGACAAGCGCTAAACGTGAAGACGATGGGA	3063	
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Qy	3064	TAA 3066		
Db	240	TAA 242		

RESULT 12
US-09-077-675A-9
; Sequence 9, Application US/09077675A

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Patent No. 6242199
GENERAL INFORMATION:
APPLICANT:  Pai, Lee-Yuh
APPLICANT:  Feigner, Scott C.
APPLICANT:  Howard, Andrew D.
APPLICANT:  Pang, Sheng-Shung
APPLICANT:  Von Der Ploeg, Leonardus H.T.
TITLE OF INVENTION:  RECEPTOR ASSAY
NUMBER OF SEQUENCES:  16
CORRESPONDENCE ADDRESS:
ADDRESS:  Merck & Co., Inc.
STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
CITY:  Rahway
STATE:  NJ
COUNTRY:  USA
ZIP:  07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE:  Diskette
COMPUTER:  IBM Compatible
OPERATING SYSTEM:  DOS
SOFTWARE:  FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/09/077,675A
FILING DATE:  3-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:  Cocuzzo, Anna L.
REGISTRATION NUMBER:  42,452
REFERENCE/DOCKET NUMBER:  19590P
TELECOMMUNICATION INFORMATION:
TELEPHONE:  732-594-1273
TELEFAX:  732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO:  9:
SEQUENCE CHARACTERISTICS:
LENGTH:  1122 base pairs
TYPE:  nucleic acid
STRANDEDNESS:  single
TOPOLOGY:  linear
MOLECULE TYPE:  cdna
US-09-077-675A-9

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Query Match	7.5%;	Score 228.8;	DB 3;	Length 1122;
Best Local Similarity	57.9%;	Pred. No. 4e-38;		
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QY	1181	CGGGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGGCGGTACCGGACATCGGCAC	1240	
DB	420	GGGTATCGTGGCAACTGCTTACCAATGCTGGTGGTGTGCGGCTTCGGGAGTGGGCAC	479	
QY	1241	CACCACAACTTGTACTCGGGCAGCATGCGCGTGTCCGACCTACTCATCTGTCTGGGCT	1300	
DB	480	CACCACAACTCTACTCTGCAGCATGGCTTCTCCGATCTGCTCATCTTCTCTGTCAT	539	
QY	1301	CGGTTTCGACCTGTACCGGCTCTGGCGCTTCGGGGCCCTGGGTGTTCCGGCCCGTGTCTCG	1360	
DB	540	GCCCTTGGACCTCTGTTGGCTCTTGGCAGTACCGGGCCCTGGAACTTCGGCGACCTCTCTCTG	599	
QY	1361	CGCCCTGTCCCTCTACGTGGGGGAGGGCTGCACCTACGCCAAGCTGCTGCATATGACCGC	1420	
DB	600	CAAACTCTTCCAAATTCGTCAGTGAGAGCTGCACCTACGCCACGGTCTCACCATCACAGC	659	
QY	1421	GCTCAGCGTCGAGCGCTACTGGGCCATCTGCGCCGCCGCTCCGGCCCGCGCTCTTGTGTAC	1480	
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720 CAAGGGGGGTGAAGCTGTGATCTTCTGCTGCTGGCGCGTGGCGCTCTGCGCGCGG 779
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; Sequence 9, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,674
; FILING DATE: 3-JUN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19589P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1122 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-077-674-9
Query Match
Best Local Similarity 7.5%; Score 228.8; DB 4; Length 1122;
Matches 424; Conservative 0; Mismatches 307; Indels 1; Gaps 1;
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Db GCTCTTCCCGCGCGCTGCTGGCGCGCTCACAGCCACCTGCGGTGACCTCTTCTGCT 419
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1080 CCGGCGTCTAT 1091
RESULT 14
US-09-077-675A-15
; Sequence 15, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.


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Job time : 506.911 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-719-485-1
Perfect score: 3066
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- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2013.2	65.7	2040	17	US-10-417-820A-151
5	1038	33.9	1161	18	US-10-679-813-11
6	901	29.4	1239	15	US-10-225-567A-472
7	901	29.4	1239	15	US-10-290-078-13
8	901	29.4	1239	15	US-10-290-078-14
9	901	29.4	1239	16	US-10-206-677-1
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c 11	761.4	24.8	1179	18	US-10-363-345A-33737

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c 13	761.4	24.8	1179	19	US-10-363-483A-33737	Sequence 33737, A
14	761.4	24.8	1179	19	US-10-363-483A-33738	Sequence 33738, A
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22	228.8	7.5	870	15	US-10-225-567A-139	Sequence 139, App
23	228.8	7.5	1122	16	US-10-303-204A-9	Sequence 9, Appl1
24	228.4	7.4	1092	16	US-10-303-204A-15	Sequence 15, Appl
25	228.4	7.4	3129	16	US-10-303-204A-14	Sequence 14, Appl
26	227.8	7.4	1088	16	US-10-303-204A-6	Sequence 6, Appl1
27	227.8	7.4	1101	15	US-10-251-385-87	Sequence 87, Appl
28	227.8	7.4	1101	15	US-10-251-385-209	Sequence 209, App
29	227.8	7.4	1101	16	US-10-276-392-22	Sequence 22, Appl
30	227.8	7.4	1101	17	US-10-305-720-1148	Sequence 1148, Ap
31	227.8	7.4	1101	18	US-10-679-813-4	Sequence 4, Appl1
32	205.2	6.7	5157	9	US-09-764-877-2605	Sequence 2605, Ap
33	205.2	6.7	5157	17	US-10-242-515-2605	Sequence 2605, Ap
34	205.2	6.7	5199	9	US-09-764-877-2607	Sequence 2607, Ap
35	205.2	6.7	5199	17	US-10-242-515-2607	Sequence 2607, Ap
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ALIGNMENTS

RESULT 1

US-09-876-252-129
; Sequence 129, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Re
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948

1 PRIOR FILING DATE: 1999-03-12
2 PRIOR APPLICATION NUMBER: 60/123,951
3 PRIOR FILING DATE: 1999-03-12
4 PRIOR APPLICATION NUMBER: 60/123,946
5 PRIOR FILING DATE: 1999-03-12
6 PRIOR APPLICATION NUMBER: 60/123,949
7 PRIOR FILING DATE: 1999-03-12
8 PRIOR APPLICATION NUMBER: 60/152,524
9 PRIOR FILING DATE: 1999-09-03
10 PRIOR APPLICATION NUMBER: 60/151,114
11 PRIOR FILING DATE: 1999-08-27
12 PRIOR APPLICATION NUMBER: 60/108,029
13 PRIOR FILING DATE: 1998-11-12
14 PRIOR APPLICATION NUMBER: 60/136,436
15 PRIOR FILING DATE: 1999-05-28
16 PRIOR APPLICATION NUMBER: 60/136,439
17 PRIOR FILING DATE: 1999-05-28
18 PRIOR APPLICATION NUMBER: 60/136,567
19 PRIOR FILING DATE: 1999-05-28
20 PRIOR APPLICATION NUMBER: 60/137,127
21 PRIOR FILING DATE: 1999-05-28
22 PRIOR APPLICATION NUMBER: 60/137,131
23 PRIOR FILING DATE: 1999-05-28
24 PRIOR APPLICATION NUMBER: 60/141,448
25 PRIOR FILING DATE: 1999-06-29
26 PRIOR APPLICATION NUMBER: 60/136,437
27 PRIOR FILING DATE: 1999-05-28
28 PRIOR APPLICATION NUMBER: 60/156,555
29 PRIOR FILING DATE: 1999-09-29
30 PRIOR APPLICATION NUMBER: 60/156,634
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32 PRIOR APPLICATION NUMBER: 60/156,653
33 PRIOR FILING DATE: 1999-09-29
34 PRIOR APPLICATION NUMBER: 60/157,280
35 PRIOR FILING DATE: 1999-10-01
36 PRIOR APPLICATION NUMBER: 60/157,294
37 PRIOR FILING DATE: 1999-10-01
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40 PRIOR APPLICATION NUMBER: 60/157,282
41 PRIOR FILING DATE: 1999-10-01
42 PRIOR APPLICATION NUMBER: 60/156,633
43 NUMBER OF SEQ ID NOS: 146
44 SOFTWARE: PatentIn version 3.0
45 SEQ ID NO 129
46 LENGTH: 2040
47 TYPE: DNA
48 ORGANISM: Homo sapiens
49 US-09-876-252-129

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2035; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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QY 1569 CAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGGCAACCGCGCGATCGCTCTCTCG 1628
Db 541 CAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGGCAACCGCGCGATCGCTCTCTCTCG 600
QY 1629 CCTCTCGCTGTGCTCGCGCTCTCTGCTCTCGGGGCGGCAACCGCGCTCCCGCGCTCG 1688
Db 601 CCTCTCGCTGTGCTCGCGCTCTCTGCTCTCGGGGCGGCAACCGCGCTCCCGCGCTCG 660
QY 1689 GGGCCCGAGACCGCGGAGCGCGCTGTTCAGCGCGCAATCCCGCGCGAGCGCGCGCG 1748
Db 661 GGGCCCGAGACCGCGGAGCGCGCTGTTCAGCGCGCAATCCCGCGCGAGCGCGCGCGCG 720
QY 1749 CAGCTGGGCGCTGCGGTCTCATGCTGTGGGTCAACACCGCTACTCTCTCTCTCTCTCTCT 1808
Db 721 CAGCTGGGCGCTGCGGTCTCATGCTGTGGGTCAACACCGCTACTCTCTCTCTCTCTCTCT 780
QY 1809 CTGTGCTCAGCATCTCTTACGGGCTCATCGGGGCGGAGCTGTGAGCAGCGCGCGCGCG 1868
Db 781 CTGTGCTCAGCATCTCTTACGGGCTCATCGGGGCGGAGCTGTGAGCAGCGCGCGCGCGCG 840
QY 1869 CTGCGAGGCGCGCGCTCGGGGCGGAGAGGCGCAACCGCGAGACCGTCCGGTCTCTG 1928
Db 841 CTGCGAGGCGCGCGCTCGGGGCGGAGAGGCGCAACCGCGAGACCGTCCGGTCTCTG 900
QY 1929 CGTAAGTGGAGCGCGCTGGTTCGTAAGACCGCTGCTGAGTCCGCGCGCGCGCGCGGAC 1988
Db 901 CGTAAGTGGAGCGCGCTGGTTCGTAAGACCGCTGCTGAGTCCGCGCGCGCGCGCGGAC 960
QY 1989 GCGCAACGCTGGGTCCCTTCCCTGCTCGCCAGCTCTGGGGCGCGCTTCCAGCTCCC 2048
Db 961 GCGCAACGCTGGGTCCCTTCCCTGCTCGCCAGCTCTGGGGCGCGCTTCCAGCTCCC 1020
QY 2049 --TCCTATTTCCAGCTTCCAGCTTCCAGCGCGGTACTTCCATCCCGAGAAACCATG 2106
Db 1021 TTTCTATTTCCAGCTTCCAGCTTCCAGCGCGGTACTTCCATCCCGAGAAACCATG 1080
QY 2107 TCCTGTCCCGAGGAGCTCTGGGGACCGCGGGCTTTGAGGGTGGATCCCGCGATC 2166
Db 1081 TCCTGTCCCGAGGAGCTCTGGGGACCGCGGGCTTTGAGGGTGGATCCCGCGATC 1140
QY 2167 CGATTTCAGTAACACGAGTGTCTTCCAGAGCTCTGAGAGCTCTGAGAGAGAGAGTGGTAA 2226
Db 1141 CGATTTCAGTAACACGAGTGTCTTCCAGAGCTCTGAGAGCTCTGAGAGAGAGAGTGGTAA 1200
QY 2227 TTTCTTAATCCAAACCTGTAGATGCGCAAAATGAGAGTCTTCCAGTGTCTTTGAGA 2286
Db 1201 TTTCTTAATCCAAACCTGTAGATGCGCAAAATGAGAGTCTTCCAGTGTCTTTGAGA 1260
QY 2287 AGACGAGGAGATTTTCAATTAAGCTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2346
Db 1261 AGACGAGGAGATTTTCAATTAAGCTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1320
QY 2347 TAAAGTAAACCTTGTCTGCTATCAAAAGTAAAGTGTGACAGCTTGTGTAGATTTCTT 2406
Db 1321 TAAAGTAAACCTTGTCTGCTATCAAAAGTAAAGTGTGACAGCTTGTGTAGATTTCTT 1380

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QY 2407 TTCAACAGAGAACAGAAAACCTTGTCTCCGAAGTGGGTTTGTGGAAGGAAAGCCTGCAAGG 2466
Db 1381 TTCAACAGAGAACAGAAAACCTTGTCTCCGAAGTGGGTTTGTGGAAGGAAAGCCTGCAAGG 1440
QY 2467 CGGCTTGTTCAGAGAAATGCTCCTTCTGGTTATGTCAGCCTTGATAACACATATGGG 2526
Db 1441 CGGCTTGTTCAGAGAAATGCTCCTTCTGGTTATGTCAGCCTTGATAACACATATGGG 1500
QY 2527 AGCCTACTATGACATGATTTTAAACAAAGATATCCATGACAGCTGTCAGCCTGTCTATTTTCT 2586
Db 1501 AGCCTACTATGACATGATTTTAAACAAAGATATCCATGACAGCTGTCAGCCTGTCTATTTTCT 1560
QY 2587 GGGGTGAGATCTGCTAGGTAGAAATTTCTCTAATTTATTTTCTGCTGTACTTGTATT 2646
Db 1561 GGGGTGAGATCTGCTAGGTAGAAATTTCTCTAATTTATTTTCTGCTGTACTTGTATT 1620
QY 2647 GCAGATGTTCTCTCGGGTGGGGGTTTATTTGCTTCCCAATGCTTTTCTTAATCCC 2706
Db 1621 GCAGATGTTCTCTCGGGTGGGGGTTTATTTGCTTCCCAATGCTTTTCTTAATCCC 1680
QY 2707 GGTGCTGTCTTATGTTGCAAGTGTGGTCTTCTGCGATTTATTAATTTGCTGTGCCC 2766
Db 1681 GGTGCTGTCTTATGTTGCAAGTGTGGTCTTCTGCGATTTATTAATTTGCTGTGCCC 1740
QY 2767 TTCCACGTTGGCAGAAATCATTTACATAAACAACGGAAGATTCGCGATGATGTACTTCT 2826
Db 1741 TTCCACGTTGGCAGAAATCATTTACATAAACAACGGAAGATTCGCGATGATGTACTTCT 1800
QY 2827 CAGTACTTTACATCGTCTGCTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATC 2886
Db 1801 CAGTACTTTACATCGTCTGCTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATC 1860
QY 2887 CTCTACAACTCATTTTCAAGAGTACAGAGCGCGGCTTTTAAACTGCTGCTGCAAGG 2946
Db 1861 CTCTACAACTCATTTTCAAGAGTACAGAGCGCGGCTTTTAAACTGCTGCTGCAAGG 1920
QY 2947 AAGTCCAGGCGAGAGGCTTCACAGAAAGCAGGACATGCGGGGGAAGTTGCAAGGAC 3006
Db 1921 AAGTCCAGGCGAGAGGCTTCACAGAAAGCAGGACATGCGGGGGAAGTTGCAAGGAC 1980
QY 3007 ACTGAGAGACACAGGCGGCTACACCGAGACAGCAGCCTTAAGTGAACAGATGGGATAA 3066
Db 1981 ACTGAGAGACACAGGCGGCTACACCGAGACAGCAGCCTTAAGTGAACAGATGGGATAA 2040
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RESULT 2

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US-10-417-820A-129
; Sequence 129, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7 US28 CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
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; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-129

Query Match 65.9%; Score 2021.2; DB 17; Length 2040;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2035; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1029 ATGGGACAGCCCTCGAAACGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1088
Db 1 ATGGGACAGCCCTCGAAACGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
QY 1089 GCGCTGCGCGCTTGGCAGACGCGCGCTGCTGCGCGCTTTTCCCTTGGGGCGCTGGTGGCG 1148
Db 61 GCGCTGCGCGCTTGGCAGACGCGCGCTGCTGCGCGCTTTTCCCTTGGGGCGCTGGTGGCG 120
QY 1149 GTGACCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208
Db 121 GTGACCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 1209 ATGCTGATCGGGCGCTACCGGGACATGCGGACACACCAACTTGTACTTGGGACGATG 1268
Db 181 ATGCTGATCGGGCGCTACCGGGACATGCGGACACACCAACTTGTACTTGGGACGATG 240
QY 1269 GCCGTGTCGACCTACTCATCTCTGCTGCGGGCTGCGCTTTCGACCTGTATCCGCTCTGG 1328
Db 241 GCCGTGTCGACCTACTCATCTCTGCTGCGGGCTGCGCTTTCGACCTGTATCCGCTCTGG 300
QY 1329 TCGGCGCGCTGGGTGTTGCGGCGCGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTG 1388
Db 301 TCGGCGCGCTGGGTGTTGCGGCGCGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTG 360
QY 1389 TGCACCTACGCGACGCTGCTGACATGACCGCGCTCAGCGTCGAGCGCTACTTGCGCCATC 1448
Db 361 TGCACCTACGCGACGCTGCTGACATGACCGCGCTCAGCGTCGAGCGCTACTTGCGCCATC 420
QY 1449 TGCGCGCGCTTCCGCGCGCGCTTCTTGTCTACCGCGCGCGCGCTTCCGCGCGCTCATCG 1508
Db 421 TGCGCGCGCTTCCGCGCGCGCTTCTTGTCTACCGCGCGCGCGCTTCCGCGCGCTCATCG 480
QY 1509 GTGCTCTGGGCGGTGGGCGCTGCTCTCTGCGCGCTGCTTCTTGTCTGCTGGGCGTTCAG 1568
Db 481 GTGCTCTGGGCGGTGGGCGCTGCTCTCTGCGCGCTGCTTCTTGTCTGCTGGGCGTTCAG 540
QY 1569 CAGACACCGCGCATCTCCGTAGTCCCGGCTCAATGCGACCGCGCGGATCGCTTCTTCG 1628
Db 541 CAGACACCGCGCATCTCCGTAGTCCCGGCTCAATGCGACCGCGCGGATCGCTTCTTCG 600
QY 1629 CCTCTCGCTCTGTCGCGCGCTTCTTGTGCTCTGCGGGCGCGCACCGCGCTTCCCGCGCT 1688
Db 601 CCTCTCGCTCTGTCGCGCGCTTCTTGTGCTCTGCGGGCGCGCACCGCGCTTCCCGCGCT 660
QY 1689 GGGCCGAGACCGCGGAGCGCGCGCTGTTTACGCGCGGAATGCGCGCGAGCGCCCGCG 1748
Db 661 GGGCCGAGACCGCGGAGCGCGCGCTGTTTACGCGCGGAATGCGCGCGAGCGCCCGCG 720
QY 1749 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1808
Db 721 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
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; ORGANISM: Homo sapiens
US-10-225-567A-472

Query Match	29.4%	Score	901	DB 15	Length	1239	
Best Local Similarity	100.0%	Mismatch	0	Mismatch	6.4e-210		
Matches	901	Conservative	0	Indels	0	Gaps	0
Qy	1029	ATGGCGAGCCCTCGAAACGGCAGCGACGGGCCCGGAGGGGGCGCGGAGCGCCGCTGCGCC	1088				
Db	1	ATGGCGAGCCCTCGAAACGGCAGCGACGGGCCCGGAGGGGGCGCGGAGCGCCGCTGCGCC	60				
Qy	1089	CGCGTCGCCGCTTCGAGAGAGCGCGCTGCTGCGCCCTTTCCCTTGGGGGGCGCTGGTGC	1148				
Db	61	CGCGTCGCCGCTTCGAGAGAGCGCGCTGCTGCGCCCTTTCCCTTGGGGGGCGCTGGTGC	120				
Qy	1149	GTGACCGCTGTGCTGTGCTGTCTGCTGCTCGGGGTGAGCGGCAACGTGGTACCGCTG	1208				
Db	121	GTGACCGCTGTGCTGTGCTGTCTGCTGCTCGGGGTGAGCGGCAACGTGGTACCGCTG	180				
Qy	1209	ATGCTGATCGGGCGCTACCGGGAATGCGGACACACCAACTTGTACTTGGGAGAGCATG	1268				
Db	181	ATGCTGATCGGGCGCTACCGGGAATGCGGACACACCAACTTGTACTTGGGAGAGCATG	240				
Qy	1269	GCCGTGTCGACCTACTCATCTGCTCGGGGTGCGCTTCGACCTGTACCGCTCTGGCGC	1328				
Db	241	GCCGTGTCGACCTACTCATCTGCTCGGGGTGCGCTTCGACCTGTACCGCTCTGGCGC	300				
Qy	1329	TCGCGGCCCTGGGTTCGCGCGCGCTGCTGTCGCGCTGTGCTTCTACGTGGGCGAGGCG	1388				
Db	301	TCGCGGCCCTGGGTTCGCGCGCGCTGCTGTCGCGCGCTGTCCCTCTACGTGGGCGAGGCG	360				
Qy	1389	TGCACCTACGCCACGCTGTGCAATGACCGCGCTCAGCGTCGAGCGCTACTTCGCCCATC	1448				
Db	361	TGCACCTACGCCACGCTGTGCAATGACCGCGCTCAGCGTCGAGCGCTACTTCGCCCATC	420				
Qy	1449	TGCGCGCGCTTCGCGCGCGCGCTGTGGTGTACCGCGCGCGCGCTCGCGCGCTCATGCT	1508				
Db	421	TGCGCGCGCTTCGCGCGCGCGCTGTGGTGTACCGCGCGCGCGCTCATGCTCATGCT	480				
Qy	1509	GTGCTCTGGGCGGTGGGCGCTGCTCTCTGCGCGCTCCCTTCTTGTCTCTGTTGGGCGT	1568				
Db	481	GTGCTCTGGGCGGTGGGCGCTGCTCTCTGCGCGCTCCCTTCTTGTCTCTGTTGGGCGT	540				
Qy	1569	CAGAACCCCGGATCTCCGTAGTCCCGGCGCTCAATGSCACGGCGGAGTCGCTCTCTCG	1628				
Db	541	CAGAACCCCGGATCTCCGTAGTCCCGGCGCTCAATGSCACGGCGGAGTCGCTCTCTCG	600				
Qy	1629	CCTCTCGCTCGTTCGCCCTCTCTGGCTCTCGGGGGGCGCACCGCGCTCCCGCGCTCG	1688				
Db	601	CCTCTCGCTCGTTCGCCCTCTCTGGCTCTCGGGGGGCGCACCGCGCTCCCGCGCTCG	660				
Qy	1689	GGGCGCGAGACCGCGGAGGCGCGCGCTGTGTACGCGCGAATGCGCGCGAGCCCGCGCG	1748				
Db	661	GGGCGCGAGACCGCGGAGGCGCGCGCTGTGTACGCGCGAATGCGCGCGAGCCCGCGCG	720				
Qy	1749	CAGCTGGGCGCGCTCGCTGTATGCTGTGGGTTCACACCGCTACTTCTCTCGCCCTTT	1808				
Db	721	CAGCTGGGCGCGCTCGCTGTATGCTGTGGGTTCACACCGCTACTTCTCTCGCCCTTT	780				
Qy	1809	CTGTGCTCTAGCATCTCTTACCGGCTCATTCGGGCGGAGCTGTGTGAGCAGCGCGCGCG	1868				
Db	781	CTGTGCTCTAGCATCTCTTACCGGCTCATTCGGGCGGAGCTGTGTGAGCAGCGCGCGCG	840				
Qy	1869	CTGGAGGCCCGCGCGCTTCGGGGCGGAGAGAGGCCACCGGACAGCGCTCGCGTCTCTG	1928				
Db	841	CTGGAGGCCCGCGCGCTTCGGGGCGGAGAGAGGCCACCGGACAGCGCTCGCGTCTCTG	900				
Qy	1929	C 1929					
Db	901	C 901					

RESULT 7

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Db 721 CAGCTGGGCGGCTGCGTGTATGCTGTGGGTACACCGGCTACTTCTTCTGCGCCCTTT 780
Qy 1809 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGGCGG 1868
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGGCGG 840
Qy 1869 CTGGAGGCGCGGCGGCTCTGGGGCGGAGAGAGGCAACCGGAGACCGTCTGGGTCTG 1928
Db 841 CTGGAGGCGCGGCGGCTCTGGGGCGGAGAGAGGCAACCGGAGACCGTCTGGGTCTG 900
Qy 1929 C 1929
Db 901 C 901

RESULT 8
US-10-290-078-14
; Sequence 14, Application US/10290078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875.
; TITLE OF INVENTION: 14395, 14618, 17692 or 58874
; FILE REFERENCE: MPI2001-288P1(M)
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-290-078-14

Query Match 29.4%; Score 901; DB 15; Length 1239;
Best Local Similarity 100.0%; Pred. No. 6.4e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1029 ATGGGAGCCCTCGAAGCGGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1088
Db 1 ATGGGAGCCCTCGAAGCGGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
Qy 1089 GCGTGGCGGCTTGGAGGAGCGGCGGCTGCGGCTTTCCCTGGGGGCGCTGTGCGG 1148
Db 61 GCGTGGCGGCTTGGAGGAGCGGCGGCTGCGGCTTTCCCTGGGGGCGCTGTGCGG 120
Qy 1149 GTGACCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208
Db 121 GTGACCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy 1209 ATGTGTATGCGGCGCTACCGGAGCATGCGGAGCAGGAGCAGGAGCAGGAGCAGG 1268
Db 181 ATGTGTATGCGGCGCTACCGGAGCATGCGGAGCAGGAGCAGGAGCAGGAGCAGG 240
Qy 1269 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGGCTTCCGCTTCCGCTTCCGCTT 1328
Db 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGGCTTCCGCTTCCGCTTCCGCTT 300
Qy 1329 TCGGGGCGCTGGGTGTTGGGGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCT 1388
Db 301 TCGGGGCGCTGGGTGTTGGGGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCT 360
Qy 1389 TGCACCTACGACAGCTGCTGACATGACCGGCTGACGCGTACGCGGCTACCTGCGCATC 1448
Db 361 TGCACCTACGACAGCTGCTGACATGACCGGCTGACGCGTACGCGGCTACCTGCGCATC 420
Qy 1449 TGCGGCGGCTTCCGCGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1508
Db 421 TGCGGCGGCTTCCGCGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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Qy 1509 GTGCTTGGGCGGCTGCTCTCTGCGGCTCCCTTCTTGTGCTTCTGCTGGGCGTCCAG 1568
Db 481 GTGCTTGGGCGGCTGCTCTCTGCGGCTCCCTTCTTGTGCTTCTGCTGGGCGTCCAG 540
Qy 1569 CAGGACCCCGGCATCTCGTAGTCCGGGCTCAATGGACACCGCGGATCGCTCTCTCG 1628
Db 541 CAGGACCCCGGCATCTCGTAGTCCGGGCTCAATGGACACCGCGGATCGCTCTCTCG 600
Qy 1629 CCTCTCGGCTGCTGCGGCGCTCTCTGCTCTCGGGGCGGCGGCGGCGGCGGCGG 1688
Db 601 CCTCTCGGCTGCTGCGGCGCTCTCTGCTCTCGGGGCGGCGGCGGCGGCGGCGG 660
Qy 1689 GGGCCCGAGACCGCGGAGCGCGGCTGTTCAGCGCGCGAATGCGGCGGAGCGGCGG 1748
Db 661 GGGCCCGAGACCGCGGAGCGCGGCTGTTCAGCGCGCGAATGCGGCGGAGCGGCGG 720
Qy 1749 CAGCTGGGCGGCTGCGGTGCTCATGCTGGGTACACCGGCTACTTCTTCTGCGCTTT 1808
Db 721 CAGCTGGGCGGCTGCGGTGCTCATGCTGGGTACACCGGCTACTTCTTCTGCGCTTT 780
Qy 1809 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGGCGGCGG 1868
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGGCGGCGG 840
Qy 1869 CTGCGAGCGCGGCGGCTCTGGGGCGGAGAGAGGCAACCGGAGACCGTCCGCTCTG 1928
Db 841 CTGCGAGCGCGGCGGCTCTGGGGCGGAGAGAGGCAACCGGAGACCGTCCGCTCTG 900
Qy 1929 C 1929
Db 901 C 901
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RESULT 9

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US-10-206-677-1
; Sequence 1, Application US/10206677
; Publication No. US2003018636A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences, Inc.
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; APPLICANT: Kulanter, Bruce G.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO
; TITLE OF INVENTION: GPCR 38, A G PROTEIN-COUPLED RECEPTOR (GPCR)
; FILE REFERENCE: 1920-1-8
; CURRENT APPLICATION NUMBER: US/10/206,677
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/250,251
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,452
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-206-677-1
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Query Match 29.4%; Score 901; DB 16; Length 1239;
Best Local Similarity 100.0%; Pred. No. 6.4e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1029 ATGGGAGCCCTCGAAGCGGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1088
Db 1 ATGGGAGCCCTCGAAGCGGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
Qy 1089 GCGTGGCGGCTTGGAGGAGCGGCGGCTGCTGCGGCTTTCCCTGGGGGCGCTGTGCGG 1148
Db 61 GCGTGGCGGCTTGGAGGAGCGGCGGCTGCTGCGGCTTTCCCTGGGGGCGCTGTGCGG 120
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Db 841 CTGGAGGCGCGCCCTCGGGGCGGAGAGAGGCCACCGGCAGACCGTCCGCGTCTGT 900
Qy 1929 C 1929
Db 901 C 901

RESULT 11

US-10-363-345A-33737/c
; Sequence 33737, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33737
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 33737
US-10-363-345A-33737

Query Match 24.8%; Score 761.4; DB 18; Length 1179;
Best Local Similarity 77.9%; Pred. No. 8.8e-176;
Matches 918; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

Qy 588 CAGATCCCTTCGAAAGTCCCGGAGTACGAGCTGACAAAGCCCGTACAGTCTCAG 647
Db 1179 CAATCCCTTCGAAATACCGGAATACCAACTAACAAAGCCCGTACAACTCAA 1120
Qy 648 TCCTGTAAACAAAGTGTCTAGGTGTCAGATCGCTCACCGGACCGGGTAGGGTCGTG 707
Db 1119 TCCTATAACCAAACTATCTAAATACAAACATCGCTCACCGAACCGAATAAACTCGTA 1060
Qy 708 CGCTAAGGCGCGGGTATTCAGTTAGTGAGAGGAAGCGCTCGGAATCGATGAGGC 767
Db 1059 CGCTAAACCGCGAATATTCATTAATAAATAAAGCCCTTAATAACTACATAAC 1000
Qy 768 CCGGAGAGGCGCGGAGCGGAGCATCGCGGCGCGGGCGCGCGCGCGTGGCGG 827
Db 999 CCGAAAAAAGCGGAAACCGAAACAAACCGAACCGAACCGGACCGTAAACGA 940
Qy 828 AGACTGCGCGAGTGTCTCGGAGCGCTCGGAGCCACCCCGAGAGCGCTTCTCGC 887
Db 939 AACTACGCGCACTAATCGAAACGCTCGAAACCCACCCCGCAACCGCTTCTCGC 880
Qy 888 CCGCGAGCGAGCGAGCGCTCGCGTGTGACTCGCGCGCGCGCGCGCGCGTGGGCT 947
Db 879 CCGCGCAACGCAACGCAACGCTCGCGTGTGACTCGCGCGCGCGCGCAACGCTGAACT 820
Qy 948 GGGAAAGAGCGGCTCACGAGAGGACCAACCGCGAGCTCCAGCCCGCGCGGACG 1007
Db 819 AAAAAAAGCGTCAACCGAAAAAAGCAACCGCGCAAACTCCCAACCGCGCGGAAACG 760
Qy 1008 CCGGCGCGCGCGGAGCAACCATGGGAGCCCTTGAACGCGAGCGAGCGCGCGCGAGGG 1067
Db 759 CGACGACCGCGGAAACACCCATAACAAACCCCTTAACACGACGACCGCGCGGAAAA 700
Qy 1068 CGCGGAGCGCGCGTGGCGCGCTGCGGCTTTCGACGAGCGCGCTGTCGCCCTTT 1127
Db 699 ACGGAAAAACCGCGCTAACCGCGCTACCGCTTACGACGAACCGCGCTACTCGCCCTTT 640
Qy 1128 CCGCTGGGGCGCTGGTCCGGTACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1187
Db 639 CCGCTAAAAACGCTAAATACCGATACCGCTATATACCTATATACCTATTCGCTCGAATA 580

Qy 1188 AGCGCAACGTTGTGACCGGTGATGCTGATCGGGCGCTACCGGGACATCGGACCAACACC 1247
Db 579 AACGACACGTAATAACCGTAATACTAATCGAACGCTACCGAAACATACGAACCAACACC 520
Qy 1248 AACTGTACCTGGGAGCATGGCGGTGTCGACACCTACTATCTCTGCTCGGGTGGCGTTC 1307
Db 519 AACTTATACCTAAACAAACATTAACCGTATCCGACCTACTCATCTACTCGAACTACCGTTC 460
Qy 1308 GACGTGTACCGCTCTGCGCGCTCGCGGCGCTGGGTGTTTCGGGCGCGCTGTCTGCGCGCTG 1367
Db 459 GACCTATACCGCTCTAACGCTCGGACCTTAATAATTTCGAACCGCTACTCTACCGCTTA 400
Qy 1368 TCCCTCTACGTGGGCGAGGGTGCACCTTACGCCAGCTGCTGCACATGACCGCGCTCAGC 1427
Db 399 TCCCTCTACGTAAACGAAACCTACACCTTACGCCAGCTACTACACATAACCGCGCTCAAC 340
Qy 1428 GTGAGCGCTACTGGCGCATCTGCGCGCGCTCGCGCGCGCTTGGTACACCGCGCGC 1487
Db 339 GTCGAACGCTACTAACCATCTACCGCGCGCTCGCGCGCGCTTAAATCACCGGACGC 280
Qy 1488 CGGTTCGCGCGCTCATCGCTGTGCTGCGCGCGCTGCTCTCTGCGCGTCCCTTC 1547
Db 279 CGGTTCGCGCGCTCATCGCTGTGCTTAAACCGTAACGCTACTCTTACCGATCCCCTTC 220
Qy 1548 TTGTTCTGTGGGCGTGCAGCAGACCCCGGCATCTCCGTAGTCCCGGCGCTCAATGCG 1607
Db 219 TTAATCTTAATAACGTCGAACAAACCCCGACATCTCCGTAAATCCCGAACCTCAATAC 160
Qy 1608 ACCGCGGAGTCCGCTCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1667
Db 159 ACCGCGGAGTCCGCTCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 100
Qy 1668 CCACGCGCTCCCGCGTCCGGGCGCGAGACCGGAGCGCGCGCTGTTACGCGCGC 1727
Db 99 CCACGCGCTCCCGCGTCCGGGCGCGAGAACCCCGAAACCGGAGCGCTATTCAACCGC 40
Qy 1728 GAATCCGCGCGAGCGCGCGCGCTGCGCGCTGCGCGCTGCGCT 1766
Db 39 GAATACCGAGCAACCCCGCGCACTAAACCGCGCTACGT 1

RESULT 12

US-10-363-345A-33738
; Sequence 33738, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33738
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 33738
US-10-363-345A-33738

Query Match 24.8%; Score 761.4; DB 18; Length 1179;
Best Local Similarity 77.9%; Pred. No. 8.8e-176;
Matches 918; Conservative 0; Mismatches 261; Indels 0; Gaps 0;
Qy 588 CAGATCCCTTCGAAAGTCCCGGAGTACGAGCTGACAAAGCCCGTACAGTCTCAG 647
Db 1 CAATCCCTTCGAAATACCGGAATACCAAAACCGGAGCGCTACTCACTCAACTCAA 60

Db 579 AACGACACGTAATAACCGTAATTAATCGAACGCTACCGAAACATACGAAACACCAACC 520
Qy 1248 AACTTGTACCTGGGAGCATGGCGGTGTCCGACCTACTCATCTGCTCGGCGTCCGTTTC 1307
Db 519 AACTTATACCTAAACAAATACCGTATCCGACCTACTCATCTTACTTCGAACCTACCGTTTC 460
Qy 1308 GACCTGTACCGCTCTTGGCGCTTCGGGCGCTTGGGTGTTCGGGCGCTGCTCTGCGGCTG 1367
Db 459 GACCTATACCGCTCTTACCGCTTCGACGCTTAAATATTCGAACCGCTACTCTACCGCTA 400
Qy 1368 TCCCTCTACGTGGGAGGCTGACCTACCGCAGCTGCTGCAATGACCGCGCTCAGC 1427
Db 399 TCCCTCTACGTAAACGAAACTACACCTACCGCAGCTACTACACATACCGCGCTCAAC 340
Qy 1428 GTCGAGGCTACCTGGCCATTCGCGCGCTTCGGCGCTTCGGTTCACCGCGGC 1487
Db 339 GTCGAACTACCTAACCATCTACCGCGCTTCGGCGCGCTTAAATACCGGAGC 280
Qy 1488 CGGTTCGCGCGCTCATCGCTGTGCTTGGGCGCTTGGGCGCTGCTCTGCGGCTCCCTTC 1547
Db 279 CGGTTCGCGCGCTCATCGCTATATCTTAAACCGTAAACGCTACTCTTACCGATCCCTTC 220
Qy 1548 TTGTTCTGTGGGCTGACGAGACCGCGCATCTCCGTAGTCCCGGGCTCAATGGC 1607
Db 219 TTATTTCTTAATAACGTTGAAACAAACCCGACATCTCCGTAATCCCGAACTCAATAAC 160
Qy 1608 ACCGCGGATCGCTCTCGCTCTCGCTCTGCGCGCTCTGCTGCTCTGCGGCGC 1667
Db 159 ACCGCGGATCGCTCTCGCTCTCGCTCTGCGCTCTGCGCGCTCTTAACTCTCGGAAACG 100
Qy 1668 CCACCGCGCTCCCGCGCTCGGAGCCGAGACCGCGGAGCGCGGCTGTTTCAGCGC 1727
Db 99 CCACCGCGCTCCCGCGCTCGAAACCCGAAACCCGAAACCCGGAACGCTATTCAACCGC 40
Qy 1728 GAATCGCGCGCGCGCGCGCTGCGGCGCTGGT 1766
Db 39 GAATACCGACCGAACCCCGCGCAACTAAACCGCTACGT 1

RESULT 14
US-10-363-483A-33738
; Sequence 33738, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33738
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-Island No: 33738
US-10-363-483A-33738

Query Match 24.8%; Score 761.4; DB 19; Length 1179;
Best Local Similarity 77.9%; Pred. No. 8.8e-176;
Matches 918; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

Qy 588 CAGATCCCTTCGAAGGTCCCGAGTACAGACTGACAAAGCGCCGTACAGTGTCTCAG 647
Db 1 CAATCCCTTCGAAATACCGGAAATACCAAAACGAAACCGCGTACAACTCA 60
Qy 648 TCCTGTAAACAAAGCTGTCTAGGTGAGACATCGCTACCGGACCGGGTAGGCTGTG 707
Db 61 TCCTATACCAAAACTATCTAAAAATACAAACATCGCTCACCAGAACCGAATAAACTCGTA 120

Qy 708 CGCTAAGGCGCGCGGCTATTTCAGTTAGTGAGAGGGAAGCGCCCTTGAACTGCATGCGC 767
Db 121 CGCTAAAAACCGCGGAATATTCCAAATTAATAAAAAAAGCGCCTAAAACTACATAAAC 180
Qy 768 CCGGAGAGGCGCGGAGCGGAGCATGGCGGCGCGGCGGCGCGGCGCGGCGGCGG 827
Db 181 CCGAAAAAAGCGCGAAAAACGAAACCGAAACCGAAACCGGACCGCGTAAACGA 240
Qy 828 AGACTGCGCGCAGCTAGCTCGGGAGCGCTCGGAGCCACCCGAGAGCGCTTCTCGC 887
Db 241 AAATCTAGCGCACTACTCGAAACCGCTTCGAAACCGACCCCGGAAACCGCTTCTCGC 300
Qy 888 GCGCGCAGCGCAGCGAGCGCTCCGCGCTGTGACTGCGCGCGCGCGAGCGTTCGGGCT 947
Db 301 GCGCGCAACGCAACGCAACGCTCCGCGCTCTAACCTACCGCGCGCGCAAGTACGAACT 360
Qy 948 GGGNAAGGAGCGCTACCGAGAGGAGGACCGCGCAGGCTCCAGCCCGGACCGGAGC 1007
Db 361 AAAAAAAGCGCTACCGAAAAAAGCGCGCGCAAACTCCCAACCCGACCGCAAAACG 420
Qy 1008 CCGCGCGCGCGGAGCACCCATGGGAGCGCCCTTGGAAACGCGAGCGCGCGCGAGGG 1067
Db 421 CGACGACCGCGGAAACACCCATTAACAAACCCCTAAACGAAACGAGCCCGCGGAAAA 480
Qy 1068 GCGCGGAGCGCGCGTGGCGCGCTGCGCGCTTTGCGACGAGCGCGCTGCTCGCCCTTT 1127
Db 481 AGCGAAAAACCGCGTAACCGCGCTACCGCGCTTTACGACGAAACGCGCTACTCGCCCTTT 540
Qy 1128 CCGCTGGGCGGCTGCTGCGGCTGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1187
Db 541 CCGCTAAAAACGCTTAATACCGATAACCGCTATATACCTATATATCTATTCGTCGGAATA 600
Qy 1188 AGCGGCAACGTGTGACCGCTGATGCTGATCGGGCGCTACCGGAGCATGCGGACCAAC 1247
Db 601 AACGACAACTGTATACCGTAATTAATCGAACGCTACCGAAACATACGAAACCAAC 660
Qy 1248 AACTTGTACCTGGGAGCATGGCGCTGTCGACACTACTCATCTGCTGCGGCTGCGGTT 1307
Db 661 AACTTATACCTAAACAACTAACCGTATCGACCTACTCATCTCTACGAACTACCGTT 720
Qy 1308 GACCTGTACCGCTCTGCGGCTCGGCGCTTGGGTGTTCGGGCGGCTGCTGCTGCGGCTG 1367
Db 721 GACCTATACCGCTCTAACGCTCGGACCTTAAATATTGAAACCGCTACTCTACCGCTA 780
Qy 1368 TCCCTCTACGTGGGAGGCTGCACCTAGCCAGCTGTGTCACATGACCGCTCAGC 1427
Db 781 TCCCTCTACGTAAACGAAACCTACACCTAGCCAGCTACTACACATACCGCGCTCAAC 840
Qy 1428 GTCGAGCGCTACCTGGCCATCTGCGCGCGCTTCGCGCGCGCTTGGTTCACCGCGCG 1487
Db 841 GTCGAACTACCTAACCATCTACCGCGCGCTTCGCGCGCGCTTAAATCACCGGAGC 900
Qy 1488 CGGTTCGCGGCTCATCGCTGCTGCGGCGTGGGCGCTGCTGCTGCGGCTGCTGCTGCT 1547
Db 901 CGGTTCGCGGCTCATCGCTACTACTTAAACCGTAACGCTACTCTCTACCGATCCCTTC 960
Qy 1548 TTGTTCTGTGGGCTGCGAGGAGCCCGGACCTCCGAGTCCCGGGCTCAATGGC 1607
Db 961 TTATTTCTTAATAACGTCGAAACAAACCCGACATCTCCGTAATCCCGAACTCAATAAC 1020
Qy 1608 ACCGCGGAGTTCGCTCTCGCTCTGCTGCGCGCTCTCTGCTGCGGCTCTCTGCTGCGGCG 1667
Db 1021 ACCGCGGAATCGCTCTCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Qy 1668 CCACCGCGCTCCCGCGCTGCGGCGCGGAGACCGCGGAGCGCGGCGCTGTTTCAGCGC 1727
Db 1081 CCACCGCGCTCCCGCGCTGAAACCCGAAACCCGAAACCCGGAACCGCTATTCAACCGC 1140
Qy 1728 GAATCGCGCGGAGCGCGCGGAGCTGGGCGCTGCT 1766
Db 1141 GAATACCGGAAACCCCGCGCAACTAAACCGCTACGT 1179

RESULT 15
US-10-363-345A-33739
; Sequence 33739, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33739
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 33739
US-10-363-345A-33739

Query Match 23.5%; Score 722; DB 18; Length 1179;
Best Local Similarity 75.8%; Pred. No. 3.8e-166;
Matches 893; Conservative 0; Mismatches 285; Indels 0; Gaps 0;
QY 589 AGATCCCTTCGAAGTGCCTGGAGTACAGACTGACAAAGCGCCGCTACAGTCTCAGT 648
DB 2 AGATTTTTCGAAGGTTCGAGTATTAGATTGATAAAGCGTTCGTATAGTGTTAGT 61
QY 649 CCGTAAACCAAGCTGTAGGTCACACATCGTCTACCGACCGGTAGGCTCGTGC 708
DB 62 TTGTAAATTAAGTGTGTAGGTTAGATATCGTTTATCGGATCGGTTAGGTTCTGTC 121
QY 709 GCTAAGGCGCGCGGTATTCAGTTAGTGGAGAGGAGCGCCCTGGAACTGCATGGGCC 768
DB 122 GTTAAGGCGTTCGGTATTTAGTTAGTGGAGAGGAGCGTTTGGAAATGATGGGTT 181
QY 769 CGGAGAGGCGCGGAGCGGAGCATGCGCGGCGCGGCGCGGCGCGCGCGCGCGCGG 828
DB 182 CGGAGAGGCGCGGAGCGGAGTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTT 241
QY 829 GACTCGCGAGTACGTACGCGGAGCGCTCGGAGCCACCCCGAGAGCGCTTCTCGCG 888
DB 242 GATTCGCGTAGTTAGTTAGTTCGAGGCGTTTCGAGTTTATTCGATAGTCTGTTTTCGCG 301
QY 889 CCCCAGCGCAGCGAGCGCTCCGCGCTCTGACCTGCGCGCGCGCGCGCGCGCGCGCG 948
DB 302 TTTCGTAGCGTAGCGTAGCGTTTCGCTGTTGATTTGTCGCGTTCGTAGCGTGGGTTG 361
QY 949 GGAAGGAGGCGCTCACCAGAGGAGACACAGCGCGAGCGCTCCAGCCCGAGCCCGGAGCG 1008
DB 362 GGAAGGAGGCGCTTATCGAGAGGATTAACGCGTTAGGTTTATGTTAGTTCGATTCGAGCGC 421
QY 1009 GCGCGCGCGCGGAGCACCATGCGACGCCCTGGAACGGAGAGCGACCGCCCGAGGGGG 1068
DB 422 GCGCGTCCGCGGAGTATTTATGGGTAGTTTTTGGAACTGGTAGCGATCGTTTCGAGGGGG 481
QY 1069 CGCGGAGCGCGCGTGGCGCGCTGCGCGCTTGGACAGCGCGCGCTGCTCGCCCTTTC 1128
DB 482 CGCGGAGTTCGTGTTGGTTTCGCTGTTGTTGCGAGAGCGTCTGTTGTTGTTT 541
QY 1129 CCCTGGGCGCGTGTGCGGTTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1188
DB 542 TTTTGGGCGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 601
QY 1189 CGCGCAAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1248
DB 602 CGCGTAACGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 661
QY 1249 ACTTGTAACCTGGGAGCATGGCGGTGCTCCGACCTACTACTACTACTACTACTACTACTACT 1308

DB 662 ATTTGTATTTCGGTAGTATGTCGTGTTTCGATTATTTATTTATTTATTTATTTATTTATTT 721
QY 1309 ACCTGTACCGCTCTGCGCTTCGCGCCCTCGGCTGTTGCGCCCTGCTGCTGCGCCCTGT 1368
DB 722 ATTTGTATCGTTTTCGGTTCGCGCTTTCGGTTCGCGCTGTTGTTGTTGTTGTTGTTGTTGTT 781
QY 1369 CCCTCTAGTGGCGAGGGCTGACCTACGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1428
DB 782 TTTTATTACGTGGCGAGGGTTGTTATTTACGTTACGTTGTTGTTGTTGTTGTTGTTGTTGTTG 841
QY 1429 TCGAGCGCTACTCGCCATCTGCGCCCTGCGCCCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTG 1488
DB 842 TCGAGCGTTATTTGTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 901
QY 1489 GCGTCCGCGCTCATCGCTGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1548
DB 902 GCGTTCGCGCTTATCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 961
QY 1549 TGTTCTGTTGGGCTGAGCAGGACCCCGCATCTCGTAGTCCCGGGCTCAATGGCA 1608
DB 962 TGTTTTCGTTGGGCTGAGTAGGATTCGCTATTTTCGTTAGTTTCGCGTTTTCGTTTTCGTTT 1021
QY 1609 CCGCGCGATCGCTCTCGCTCTCGCTCTCGCTCTCGCTCTCGCTCTCGCTCTCGCTCTCGCTCT 1668
DB 1022 TCGCGCGATCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTT 1081
QY 1669 CACCGCGCTCCCGCTGCGGCGCCGAGACCGCGAGGCGCGCGCTGCTGCTGCTGCTGCTGCTG 1728
DB 1082 TATCGTCTGTTTTCGCTGCGGGTTCGAGATCGCGAGGTCGCGCGCTGTTGTTAGTCGCG 1141
QY 1729 AATCGCGCGAGCCCGCGCAGCTGGGCGCGCTGCGT 1766
DB 1142 AATGTCGCTGAGTTTCGCTAGTTGCGCGCTGCGT 1179

Search completed: April 11, 2005, 21:00:19
Job time : 1795.07 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:51:20 ; Search time 12160.1 Seconds
(without alignments)
9597.380 Million cell updates/sec

Title: US-09-719-485-1
Perfect score: 3066
Sequence: 1 ttgaattatctgtcactg.....acgtgaagacgatgggataa 3066

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	693.8	22.6	843	5	BUS53576
2	576	18.8	590	2	BF513101 UI-H-BW1-
3	509	16.6	509	7	CR747135 CR747135
4	490.2	16.0	495	2	BF512085 UI-H-BW1-
5	360.6	11.8	399	8	AQ939773 NR5-116R
6	255.8	8.3	425	8	AQ138681 HS_3073 A
7	231.6	7.6	1046	9	AY407666 Mus muscu
8	230.4	7.5	688	7	CO959476 AGENCOURT
9	230	7.5	4435	3	AK049671 Mus muscu
10	227.8	7.4	640	6	CD618070
11	227.8	7.4	640	6	CD618071
12	227.8	7.4	1052	9	AY407664
13	226.8	7.4	500	2	BF603623
14	225.2	7.3	637	6	CD618076
15	219.2	7.1	608	6	BY724644
16	213.2	7.0	969	9	AY407665 Pan trogl
17	204	6.7	370	5	BX485214 DKF2p686E
18	203.8	6.6	635	6	CD618069
19	202.2	6.6	576	6	CD618067
20	200.8	6.5	489	1	AL042230
21	198.2	6.5	2669	3	BC035179 Homo sapi
22	197.8	6.5	606	5	BQ778458
23	197.8	6.5	619	5	BX505458 DKF2p686E
24	197.8	6.5	712	6	CD246087 AGENCOURT

25	197.8	6.5	721	6	CD364665
26	197.8	6.5	722	7	CN263776
27	197.8	6.5	779	6	CA442904
28	197.2	6.4	974	5	BX370686
29	196.8	6.4	639	5	BM992802
30	196.6	6.4	391	1	AI569401
31	196.2	6.4	656	6	CA420015
32	196	6.4	741	9	AG113248
33	196	6.4	3204	3	HSB04305
34	195.2	6.4	337	5	BUS566980
35	194.8	6.4	457	2	BF939646
36	193.6	6.3	416	6	CD520893
37	193.4	6.3	353	1	AV657198
38	193.4	6.3	854	8	AQ747659
39	193.2	6.3	643	6	CD618077
40	193	6.3	537	8	AQ322719
41	193	6.3	739	8	AQ035003
42	192.6	6.3	486	4	BG231842
43	192.6	6.3	624	6	CA423118
44	192.6	6.3	691	6	CD243422
45	192.6	6.3	853	4	BI084622

ALIGNMENTS

RESULT 1
BUS53576
LOCUS BUS53576 843 bp mRNA linear EST 16-SEP-2002
DEFINITION AGENCOURT_10242213 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:6577973 5', mRNA sequence.
ACCESSION BUS53576
VERSION BUS53576.1 GI:22903848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCES
1 (bases 1 to 843)
NIH-MGC <http://mgc.nci.nih.gov/>.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM2778 row: p column: 05
High quality sequence stop: 534.
Location/Qualifiers
1. 843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6577973"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 22.6% Score 693.8 DB 5 Length 843

QY 2043 GCTCCC--TCCATTTTCGATTCCAGCTCCACCCCGCGGTACTTCCCATATCCCCGAGAAA 2100
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 Db 181 GCTCCCTTTCTTATTTTCGATTCCAGCTCCACCCCGCGGTACTTCCCATATCCCCGAGAAA 240
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 QY 2101 ACCATGTCCTGTCCTCCAGGAGCTCTGGGGGACCCACAGGGCGCTTTGAGGGTGGGATCCC 2160
 |||||
 Db 241 ACCATGTCCTGTCCTCCAGGAGCTCTGGGGGACCCACAGGGCGCTTTGAGGGTGGGATCCC 300
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 QY 2161 CGGATCCGATTTCAGTAACACAGCAGTGCCTTTTCCAGAGCTCTTGAGACCAGAAAGGAGAGT 2220
 |||||
 Db 301 CGGATCCGATTTCAGTAACACAGCAGTGCCTTTTCCAGAGCTCTTGAGACCAGAAAGGAGAGT 360
 |||||
 QY 2221 TGGTAATTTCTTAATCAACACCTGTTAGATGCCACAAATGAGGAGTCTCTACAGTGTCTC 2280
 |||||
 Db 361 TGGTAATTTCTTAATCAACACCTGTTAGATGCCACAAATGAGGAGTCTCTACAGTGTCTC 420
 |||||
 QY 2281 TTGAGAACAGCAGGAGAGATTCATTAAAGCTAAATATTTTATTTAATGTTAAGTGATGCT 2340
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 Db 421 TTGAGAACAGCAGGAGAGATTCATTAAAGCTAAATATTTTATTTAATGTTAAGTGATGCT 480
 |||||
 QY 2341 GAAGCTTAAAGTAAACCTTGTCTGATCAAAAAGTAAAGATTTGTGCAGACCTGTTGTAGA 2400
 |||||
 Db 481 GAAGCTTAAAGTAAACCTTGTCTGATCAAAAAGTAAAGATTTGTGCAGACCTGTTGTAGA 540
 |||||
 QY 2401 ATTCTTTTCAACAGAGACAGAAAACTTGTCTCCGAAGTGGGTTTGTGGA 2450
 |||||
 Db 541 ATTCTTTTCAACAGAGACAGAAAACTTGTCTCCGAAGTGGGTTTGTGGA 590
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RESULT 3

CR747135/c
 LOCUS CR747135 NCI CGAP Sub7 509 bp mRNA linear EST 30-AUG-2004
 DEFINITION IMAGE:3070549 5', mRNA sequence.

ACCESSION CR747135

VERSION CR747135

KEYWORDS EST.

SOURCE CR747135.1 GI:51660528

ORGANISM Homo sapiens (human)

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,B.,

Peters,M., Radeflof,U. and Schneider,D.

I.M.A.G.E. cDNA Clone Collection

Unpublished (2004)

Contact: Inge Ariart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

RZPD: IMAGp9981147713.

RZPDLIB: I.M.A.G.E. cDNA Clone Collection;

Contact: Inge Ariart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel.: +49 30 32639 100

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13r, Primer sequence: TTTCCACAGGAAACAGCTATGAC.

Location/Qualifiers

1. 509

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGp9981147713 ; IMAGE:3070549"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP Sub7"

/note="Vector: pRTT3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not 1; Site 2: Eco RI; NCI CGAP Sub7

is a subtracted library derived from NCI CGAP Sub6. The

NCI CGAP Sub7 library had 12 million recombinants. A single-stranded DNA preparation of NCI CGAP Sub6 was used as a tracer in a subtractive hybridization with a driver comprising the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clones 1323378-1323911, 1456008-1456775, 1500552-1502855); NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clones 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI CGAP LUS pool 1 LLAM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI CGAP Br22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP Colo pool 1 LLAM 2644-2653, 2871-2872 (IMAGE Clones 1057416-1061255, 1144584-1145351). (6% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE Clones 2708616-2710535) and NCI CGAP Sub2 (IMAGE Clones 2710536-2712455) (4% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE Clones 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE Clones 2723592-2729346) (40% of the driver population), plus a pool of 4032 clones from NCI CGAP Sub6 (IMAGE Clones 2728969-2733190) (40% of the driver population). Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806."

ORIGIN

Query Match 16.6%; Score 509; DB 7; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3 4e-69;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2255 ACAATGAGGAGTCTCACAGTGTCTTGAGAACAGGAGGAGATTTCAATTAAGCTAAAA 2314
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 Db 509 ACAATGAGGAGTCTCACAGTGTCTTGAGAACAGGAGGAGATTTCAATTAAGCTAAAA 450
 |||||
 QY 2315 TTTTATTTAATGTTAAGTGATCTGAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAG 2374
 |||||
 Db 449 TTTTATTTAATGTTAAGTGATCTGAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAG 390
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 QY 2375 TAAAGATTGTCAGACCTGTTGTAGAATCTTTTCAACAGAGAACAGAAAACTTGTCTCTCC 2434
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 Db 389 TAAAGATTGTCAGACCTGTTGTAGAATCTTTTCAACAGAGAACAGAAAACTTGTCTCTCC 330
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 QY 2435 GAAGTGGGTTTGTGGAAGGAGCCTGCCAAGCGCGCTTGTTCAGAGAAATTTGCTCTCTCT 2494
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 Db 329 GAAGTGGGTTTGTGGAAGGAGCCTGCCAAGCGCGCTTGTTCAGAGAAATTTGCTCTCTCT 270
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 QY 2495 GGTATATGTCAGCCTTGATTAACATATGGAGCCTACTATGCAAGTTTAAAGCAAGTA 2554
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 Db 269 GGTATATGTCAGCCTTGATTAACATATGGAGCCTACTATGCAAGTTTAAAGCAAGTA 210
 |||||
 QY 2555 TCCATGAGCCTGCAGCCTGCTCAATTTTCTGGGTGAGGATCTGCCCTAGTAGAAGTT 2614
 |||||
 Db 209 TCCATGAGCCTGCAGCCTGCTCAATTTTCTGGGTGAGGATCTGCCCTAGTAGAAGTT 150
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 QY 2615 TTCTCTAATTTTATTTGCTGTACTTGTATTTATTCAGATGTTTCTTGTGCGGGGTGGGGG 2674
 |||||
 Db 149 TTCTCTAATTTTATTTGCTGTACTTGTATTTATTCAGATGTTTCTTGTGCGGGGTGGGGG 90
 |||||
 QY 2675 TTTATTTGCTTCCCAATGCTTTTGTAAATCCCGTCTGTGCTCTATGTTTCAGTGGTGG 2734
 |||||
 Db 89 TTTATTTGCTTCCCAATGCTTTTGTAAATCCCGTCTGTGCTCTATGTTTCAGTGGTGG 30
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 QY 2735 TGGTCTTGGCATTATTAATTTGCTGGTTG 2763
 |||||
 Db 29 TGGTCTTGGCATTATTAATTTGCTGGTTG 1


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RESULT 4
BF512085/c
LOCUS
DEFINITION
  BF512085 UI-H-BW1-ami-e-11-0-UI-s1 NCI CGAP Sub7 Homo sapiens cDNA clone
  IMAGE:3070172 3', mRNA sequence.
ACCESSION
  BF512085
KEYWORDS
  EST.
SOURCE
  BF512085.1 GI:11597297
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 495)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
JOURNAL
  Contact: Robert Strausberg, Ph.D.
  Email: cgapsb@mail.nih.gov
COMMENT
  Oligo-dT track not found, Not 1 site shown in beginning of sequence
  is likely internal to the message. cDNA Library Preparation: M.B.
  Soares Lab Clone distribution: NCI-CGAP clone distribution
  information can be found through the I.M.A.G.E. Consortium/LNL at:
  www-bio.lnl.gov/bbrp/image/image.html The following repetitive
  elements were found in this cDNA sequence: 190-253,
  >GC-rich#Low complexity
  Seq primer: M13 Forward
  POLYA=No.

Location/Qualifiers
  1..495
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  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:3070172"
  /lab_host="DH10B (Life Technologies)"
  /clone_lib="NCI CGAP Sub7"
  /note="Vector: pTY73D-Pac (Pharmacia) with a modified
  polylinker; Site 1: Not 1; Site 2: Eco RI; NCI CGAP Sub7
  is a subtracted library derived from NCI CGAP Sub6. The
  NCI CGAP Sub7 library had 12 million recombinants. A
  single-stranded DNA preparation of NCI CGAP Sub6 was used
  as a tracer in a subtractive hybridization with a driver
  comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM
  3334-3337, 3682-3683, 3798-3803) (IMAGE Clones
  1322376-1323911, 1456008-1456775, 1500552-1502855);
  NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
  (IMAGE Clones 1323912-1325831, 1471368-1472903,
  1492104-1493255); NCI CGAP Lu5 pool 1 LLAM 3575-3582,
  3851-3854 (IMAGE Clones 1414920-1417991,
  1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167,
  3716-3720, 3733-3735 (IMAGE Clones
  1257096-1258631, 1469064-1470983, 1475592-1476743);
  NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068
  (IMAGE Clones 985608-986759, 1101192-1101959,
  1217928-1220615); NCI CGAP Co10 pool 1 LLAM 2644-2653,
  2871-2872 (IMAGE clones
  1057416-1061255, 1144584-1145351). (6% of the driver
  population), plus a pool of 3,840 arrayed clones from
  NCI CGAP Sub1 (IMAGE Clones 270816-2710535) and
  NCI CGAP Sub2 (IMAGE Clones 2710536-2712455) (4% of
  the driver population), plus a pool of 11,136 clones from
  NCI CGAP Sub3 (IMAGE Clones 2712456-2723591) (10% of
  the driver population), plus a pool of 5,472 clones from
  NCI CGAP Sub4 (IMAGE Clones 2723592-2729326) (40% of the
  driver population), plus a pool of 4032 clones from
  NCI CGAP Sub6 (IMAGE Clones 2728969-2733190) (40% of the
  driver population). Subtraction was performed as
  previously described [Bonaldo, Lennon & Soares (1996):
  Normalization and Subtraction: Two Approaches To
  Facilitate Gene Discovery. Genome Research 6, 791-806.
  TAG_SEQ=None found"

FEATURES
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LOCUS
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  sequence.
  AO939773
  VERSION
  AO939773.1 GI:7216151
  KEYWORDS
  GSS.
  SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 399)
REFERENCE
  Zabarovsky, E.R., Gizatullin, R., Podowski, R.M., Zabarovska, V.V.,
  Xie, L., Muravenko, O.V., Kozyrev, S., Petrenko, L., Skobeleva, N.,
  Li, J., Protodopov, A., Kashuba, V., Ernberg, I., Winberg, G. and
  Wahlestedt, C.
  Nucleic Acids Res. 28 (7), 1635-1639 (2000)
JOURNAL
  MEDLINE
  PUBMED
  COMMENT
  Contact: Podowski RM
  Center for Genomics Research
  Karolinska Institute
  17177 Stockholm, Sweden
  Tel: +46-8-728-6372
  Fax: +46-8-337983
  Email: Raf.Podowski@cgr.ki.se
  Class: NotI site.
  Location/Qualifiers
    1..399

FEATURES
  source
    1..399

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"

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Query Match      11.8%; Score 360.6; DB 8; Length 399;
Best Local Similarity 96.2%; Pred. No. 3.9e-46;
Matches 380; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

624 CAAAGCCCGCTACAGTCTCAGTCTGTAAACCAAGCTGTCTAGGTTGAGACATCGC 683
395 CAAAGCCCGCTACAGTCTCAGTCTGTAAACCAAGCTGTCTAGGTTGAGACATCGC 336
694 TCACCGGACCGGTAGGCTCTGTCGCTAAGCGCGCCGGTA-TTCCAGTTAGTGGAG 742
335 TCACCGGACCGGTAGGCTCTGTCGCTAAGCGCGCCGGTATTTCAGTTAGTGAAG 276
743 GGAAGCCCTGGAACTGCATGGCCCGGAGAGCGCGGAGCGGAGCATGCGCGGC 802
275 GGAAGCCCTGGAACTGCATGGCCCGGAGAGCGCGGAGCGGAGCATGCGCGGC 216
803 CGGGCGCGCGCGCGCTGCGCGAGACTGCGCGAGCTAGCTCGGAGCGCTCGGAG 862
215 CGGGCGCGCGCGCGCTGCGCGAGACTTGGCGAGCTAGCTCGGAGCGCTCGGAG 156
863 CCCACCCCGAGAGCGCTTCTCGCGCCCGCGAGCGCGAGCGCTCCCGCTCGAC 922
155 CCCACCCCGAGAGCGCTTCTCGCGCCCGCGAGCGCGAGCGCTCCCGCTCGAC 96
923 CTGCGCGCGCGAGCGCTGCGGCTGGGAAAGAGGCGCTCACCAGAGGACCGCGGC 982
95 CTGCGCGCGCGAGCGCTGCGGCTGGGAAAGAGGCGCTCACCAGAGGACCGCGGC 36
983 CAGGCTCCCGAGCGCGAGCGCGGAGCGCGCGCGC 1017
35 CAGGCTCCCGAGCGCGAGCGCGGAGCGCGCGCGC 1

RESULT 6
A0138681
LOCUS
DEFINITION HS_3073_A2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=4 Row=G, genomic survey sequence.
ACCESSION A0138681.1 GI:3529334
VERSION A0138681
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3073 row: G column: 4
Class: BAC ends
High quality sequence stop: 425.
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"

ORIGIN
Query Match      8.3%; Score 255.8; DB 8; Length 425;
Best Local Similarity 94.2%; Pred. No. 7.1e-30;
Matches 274; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

2397 TAGAATCTCTTTCAACAGAGAACAAACCTTGTCTCCGAAGTGGTTTGTGAAGGAAG 2456
51 TCGAATCTCTTTCAACAGAGAACAAACCTTGTCTCCGAAGTGGTTTGTGAAGGAAG 110
2457 CCTCCAGAGCGCTTGTTCAGAGAAATGCTCTCTCTGTTATGTCACGCTTGATAA 2516
111 CCTCCAGAGCGCTTGTTCAGAGAAATGCTCTCTCTGTTATGTCACGCTTGATAA 170
2517 CACATATGGAGCGCTTGTTCAGAGAAATGCTCTCTCTGTTATGTCACGCTTGATAA 2576
171 CACATATGGAGCGCTTGTTCAGAGAAATGCTCTCTCTGTTATGTCACGCTTGATAA 230
2577 CATTTTCTGGGCTGAGGATCTCCCTAGGTAGAGTTTCTCTAAATTTATTTGCTGTT 2636
231 CATTTTCTGGGCTGAGGATCTCCCTAGGTAGAGTTTCTCTAAATTTATTTGCTG-T 289
2637 ACTTGTATTGACAGATGTTCTTGTGCGGCTGGGGTATTTATTTGCTTCC 2687
290 ACTTGTATTGACAGATGTTCTTGTGCGGCTGGGGTATTTATTTGCTTCCC 340

RESULT 7
A0407666
LOCUS
DEFINITION Mus musculus GHSR gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION A0407666
VERSION A0407666.1 GI:39763637
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1046)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source
1..1046
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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gene

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MEDLINE
PUBMED
REFERENCE
AUTHORS

20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, H., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

TITLE
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed sequencer

Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4

TITLE
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

JOURNAL
PUBMED
REFERENCE
AUTHORS

Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5

TITLE
The FANTOM Consortium and the RIKEN Genome Exploration Research Group, Phase I & II Team.

JOURNAL
PUBMED
REFERENCE
AUTHORS

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4435)

Adachi, J., Aizawa, K., Akimura, T., Arai, K., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kohji, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitho, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shbata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp).
URL: http://genome.gsc.riken.jp/; Tel: 81-45-503-9222, Fax: 81-45-503-9216

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES
source
1. 4435
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:C530020122"
/db_xref="taxon:10090"
/clone="C530020122"
/tissue_type="spinal cord"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
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WVTPVNFGLLCKLFOVSESTYATVLTITLSSVFAIFCPPLAKVVTGRVK
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FFVLPVCLTVLYSLIGKWRGRDAAVSSLRDQNHQTVKMLAVVFAFLICWLP
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ORIGIN

Query Match 7.5%; Score 230; DB 3; Length 4435;
Best Local Similarity 68.6%; Pred. No. 4e-26;
Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 1120 GCGCTTTCCCTCGGGCGCGCTGTCGCGGTGACCGCTGTCGCTGTCGCTGTCGCTG 1179
DB 355 CACTGTTCCCGCGCGCTGTCGCGGCGCTCACTGCCACCTGCGGCGCTTCTCGTGG 414
QY 1180 TCGGGGTGAGCGCAACGTCGTCACCTGCTCACCATGTCGCTGTCGCTGTCGCTG 1239
DB 415 TGGGCATCTCGGGCAACCTGCTCACCATGTCGCTGTCGCTGTCGCTGTCGCTG 474
QY 1240 CCACACCACTTGTACTTGGGAGCATGCGCGTGTCCGACCTACTACTTCTGCTGGGC 1299
DB 475 CCACACCACTTGTACTTGGGAGCATGCGCGTGTCCGACCTACTACTTCTGCTGGGC 534
QY 1300 TGCGCTTTCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCTGTCGCTGTCGCTG 1359
DB 535 TGCGCTGTCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCTGTCGCTGTCGCTG 594
QY 1360 GCGCGCTTTCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTG 1419
DB 595 GCGCGCTTTCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTG 654
QY 1420 CGCTCAGGCTCGAGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCTG 1479
DB 655 CGCTCAGGCTCGAGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCTG 714
QY 1480 CCGCGCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCTG 1539
DB 715 CCAAGGCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTGTCGCGCTG 774
QY 1540 GTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1581
DB 775 GGCCCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 816

RESULT 10
CD618070/c
LOCUS
DEFINITION
56030361H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION
CD618070
VERSION
CD618070.1 GI:40266335
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 640)
AUTHORS
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL
Genomics 84 (1), 205-210 (2004)
COMMENT
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1. .640
/organism="Homo sapiens"
/mol_type="mRNA"


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/gene="GHSR"  
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ORIGIN

[illegible]

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LOCUS	269181 MARC	3BOV Bos taurus	cdna 5', mRNA sequence.
DEFINITION	BF603623		
ACCESSION	BF603623		
VERSION	BF603623.1	GI:11701421	
KEYWORDS	EST.		
SOURCE	Bos taurus	(cow)	
ORGANISM	Bos taurus		

REFERENCE

AUTHORS

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W., Rohrer, G.A., Chitko-Mckown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

TTTT.F

JOURNAL
Genome Res. 11 (4), 626-630 (2001)

MEDLINE

11282978	Contact: Smith TPL
	USDA, ARS, US Meat Animal Research Center
	PO Box 166, Clay Center, NE 68933-0166, USA
	Tel: 402 762 4366
	Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing, bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 49 row: I column: 6
Seq primer: ATTTAGTGTACATATAG.

FEATURES

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/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/notes="Vector: pCMV SPORTS; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

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ORIGIN

Query Match	7.4%; Score 226.8; DB 2; Length 500;
Best Local Similarity	68.2%; Pred. No. 2.2e-25;
Matches 315; Conservative	0; Mismatches 147; Indels 0; Gaps 0;
QY	1120 CGCCCTTTCCCTGGGGCGCTGGTGGCGGTGACCGCTGTGTGCGCTGTGCTGTGCTGTGCTCG 1179
DB	39 CCCTCTTTCCCGCGCGCTGTGGCGGGCGTCACAGCCACCTGGGTGGCGCTCTTCGTGG 98
QY	1180 TCGGGGTGAGCGGCAACGTGTGACCGTGATGCTGATCGGGCGGTACCGGGACATGCGGA 1239
DB	99 TGGGCATCGGGGCAACCTGCTCACCATGCTGTGTGTGTCGCGTTTCGCGAGCTGGGTA 158
QY	1240 CCACCACCAACTTGTAACCTGGGGCAGATGCGCCGTGTCCGACCTACTCATCTCTCTCGGGC 1299
DB	159 CCACGACCAACCTCTTACCTGTCCAGCATGGCCCTCTCCGACTTACTCATCTTCTCTGCA 218
QY	1300 TGCCGTTTCGACCTGTACCGCCTCTGCGGCTTCGCGGCCCTGGGGTGTGGGGCCGCTGTCT 1359
DB	219 TGCCCTTCGACCTCGTGTGCGCTCTGGCAATTACCGGCCCTGGAACTTTGGGGCAGCCTGTCT 278
QY	1360 GCCGCTGTCCCTCTACGTGGGGAGGGGTGCACCTACGCCACGCTGCTGCACATGACCG 1419
DB	279 GCAACTCTTCAGTTTGTACGCGAGCTGCACTTACGCTACGGTCTCACCATCACCG 338
QY	1420 CGCTCAGCTCGAGCGCTACCTGGCCATCTGCCGCCGCTCGCGGCCGCGCTTGTGTCA 1479
DB	339 CGTGTAGCGTCGAGCGCTACTTCCCATCTGCTTCCGCTTCGCGGGCAGAGTGTGTATCA 398
QY	1480 CCCGGCGCGGTCGCGGCGCTCATCGCTGTGCTCTGGGCGGTGGGCGCTGCTCTCTCGCG 1539
DB	399 CCAGGGCCGGGTGAAGCTGTCATCTGTGTCACTTGGGCCGTGGCTTCTGAGCGCCG 458
QY	1540 GTCCCTCTTGTTCCTGGTGGCGTCCAGCAGACCCCGCA 1581
DB	459 GGCCCATCTTCGTGCTGTGTGGAGTGGGATCAGAAATGCA 500

RESULT 14

CD618076/c	CD618076	637 bp	mRNA	linear	EST 12-JAN-2004
LOCUS	56030461H1	FLP Homo sapiens	cdNA, mRNA	sequence.	
DEFINITION	CD618076				
ACCESSION	CD618076.1	GI:40266341			
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 637)				
AUTHORS	Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.				
TITLE	Circular rapid amplification of cdNA ends for high-throughput extension cloning of partial genes				
JOURNAL	Genomics 84 (1), 205-210 (2004)				
COMMENT	Contact: Fu GK				

Primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATCTCGAGTTAATTAATCCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified phagescript KS(+) after bulk excision from Lambda
FLC I."

ORIGIN

```
Query Match      7.1%; Score 219.2; DB 6; Length 608;
Best Local Similarity 70.3%; Pred. No. 3.1e-24;
Matches 293; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Qy 1165 TGTGCTGTTGCTGCGGTGAGCGGACAGTGGTGACCGTGATGCTGATCGGGCGCT 1224
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2 TGGCGCTCTTCTGTTGGGCATCTCGGGCAACCTGCTCACCATGCTGGTGGTTCCTCGCT 61

Qy 1225 ACCGGACATCGGACACCAACCACTTGTTACCTGGGAGCATGGCCGCTGCCGACCTAC 1284
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
62 TCCGGAGCTGGGACACCAACCAACCTTCTACCTATCCAGCATGGCCTTCTCCGATCTGC 121

Qy 1285 TCATCTGCTCGGGTGCCTGTTGACCTGTACCGCTCTGGCGCTCGCGGCCCTGGGTGT 1344
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
122 TCATCTTCTGTCATGCCGCTGGACCTCGTCCGCTCTGGCAGTATCGGCCCTGGAACT 181

Qy 1345 TCGGGCCGCTGCTGCGCGCTGTCCCTCTAGTGGGGAGGGCTGCACCTACGCCAGCG 1404
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
182 TCGGCGACCTGCTCTGCAAACTCTTCCAGTTTGTACGCGAGAGCTGCACCTACGCCAGG 241

Qy 1405 TGCTGCACATGACCGCGCTCAGCGTCGAGCGCTACCTGGCCATCTGCCGCCGCTCCGCG 1464
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
242 TCCTCACCATCACCGCGTGAGCGTCGAGCGCTACTTCGCCATCTGCTTCGCGTGGGG 301

Qy 1465 CCGCGTCTTGGTACCCGCGCGCGGTCGCCGCGCTCATCGCTGTGCTTGGGCGGTGG 1524
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
302 CCAAGGTGGTGTCAACCAAGGCGGTGTGAAGTGGTCACTCTTGTCTATTTGGGCGGTGG 361

Qy 1525 CGCTGCTCTTGCCTGCTGCTTCTTGTTCCTGGTGGGGCTGAGCAGACCCCGGCA 1581
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
362 CTTCTGAGCGCGGGGCCATCTTCNTGCTGGTGGGCGTGGAGCAGAGAACCGCA 418
```

Search completed: April 11, 2005, 12:57:47
Job time : 12166.1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:44:49 ; Search time 662.25 Seconds
(without alignments)
11075.206 Million cell updates/sec

Title: US-09-719-485-2
Perfect score: 1239
Sequence: 1 atgggcagccctcggaacgg.....acgtgaagacatgggataa 1239

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239	100.0	1239	3	Aaz45403 CDNA enco
2	1239	100.0	1239	4	Aaf85449 Nucleotid
3	1239	100.0	1239	4	Aaf85449 Nucleotid
4	1239	100.0	1239	6	Abk90132 DNA enco
5	1239	100.0	1239	8	Abz42842 Human mot
6	1239	100.0	1239	12	Adn11760 Human mot
7	1239	100.0	1239	12	Ado30072 Human GPC
8	1239	100.0	1239	12	Adq37920 Human G-p
9	1239	100.0	1506	4	Aai66989 Human GPR
10	1078	87.0	1390	3	Aaz45404 CDNA enco
11	915.6	73.9	1203	4	Aaf85448 Nucleotid
12	901	72.7	1161	4	Aaf83684 Short for
13	901	72.7	1161	12	Adn11762 Human mot
14	901	72.7	3066	3	Aaz45402 Genomic s
15	901	72.7	110000	10	Adg70447 Human ANG
16	901	72.7	110000	10	Abz79565 CLLD8 and
17	896.2	72.3	2040	3	Aaa46116 Human G p
18	896.2	72.3	2040	12	Adg86490 Human ngp
19	896.2	72.3	2040	12	Adp20283 Human GPC
20	891.4	71.9	2040	12	Adg86512 Human orp

21	546	44.1	813	4	Aaf85447 Nucleotid
c	501.2	40.5	1179	6	Abq47146 Oligonuc1
22	501.2	40.5	1179	6	Abq47147 Oligonuc1
c	437.2	35.3	1179	6	Abq47149 Oligonuc1
24	437.2	35.3	1179	6	Abq47148 Oligonuc1
25	283	22.8	283	2	Aav28290 Galanin r
26	283	22.8	283	2	AAV32651 Galanin r
27	283	22.8	283	2	AAV32651 Galanin r
28	283	22.8	283	2	AAV4930 Galanin r
29	283	22.8	283	2	AAV4930 Galanin r
30	264.8	21.4	1092	3	Aaz45405 DNA enco
31	264.8	21.4	1092	4	Aaf85450 Nucleotid
32	255.8	20.6	1050	3	Aaz61492 CDNA enco
33	234.8	19.0	1063	2	AAZ61492 Swine gro
34	234.8	19.0	1063	2	AAZ61492 Swine gro
35	233.2	18.8	1029	2	AAZ61492 Swine gro
36	233.2	18.8	1029	2	AAZ61492 Swine gro
37	231.6	18.7	1095	3	Aaz45405 DNA enco
38	231.6	18.7	1095	3	Aaz45405 DNA enco
39	230	18.6	1092	12	Ado29027 Mouse nov
40	229.8	18.5	1092	4	AAH27800 Rat growt
41	229	18.5	250	10	ACA55761 Pig signa
42	229	18.5	250	12	ADI55557 Human pol
43	228.8	18.5	870	8	ABZ42674 Human gro
44	228.8	18.5	1122	2	AAZ68665 Human gro
45	228.4	18.4	3129	2	AAZ68665 Human gro

ALIGNMENTS

RESULT 1					
AAZ45403					
ID	AAZ45403	standard;	CDNA;	1239	BP.
XX	AAZ45403;				
AC	AAZ45403;				
XX	27-MAR-2000	(first entry)			
DT	27-MAR-2000	(first entry)			
DE	CDNA encoding the motilin receptor splice variant MTL-RIA.				
XX	Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;				
KW	spliced form; MTL-RIA; MTL-R1B; gastric motility disorder;				
KW	functional defect; neurological disorder; scleroderma; colonoscopy;				
KW	paraneoplastic syndrome; radiation induced dysmotility; diabetes;				
KW	infection; stress-related motility disorder; psychogenic disorder;				
KW	gastroparesis; gastro-oesophageal reflux disease; constipation;				
KW	chronic idiopathic pseudo obstruction; acute faecal impaction;				
KW	postoperative ileus; gallstones; infantile colic; diarrhoea;				
KW	irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;				
XX	endoscopy; duodenal intubation; ds.				
OS	Homo sapiens.				
XX	Key	Location/Qualifiers			
FT	CDS	1..1239			
FT		/*tag= a			
FT		/product= "MTL-RIA"			
XX					
XX	WO9964436-A1.				
XX	16-DEC-1999.				
XX	08-JUN-1999;	99WO-US012773.			
XX	12-JUN-1998;	98US-0089098P.			
XX	(MERI) MERCK & CO INC.				
XX	Feighner SD, Patchett AA, Tan C, Mckee K, Macneil D, Howard AD;				
XX	Pong S, Smith RG;				
XX	WPI; 2000-105868/09.				
XX	P-PSDB; AAY54145.				

XX Novel receptor protein for screening compounds used in treating irritable
PT bowel syndrome, constipation and other gastric conditions.
XX Claim 4; Fig 2; 44pp; English.
XX The present sequence encodes splice variant MTL-R1A of the motilin
CC receptor. The gene encodes a G-protein coupled receptor, and is
CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A
CC (see AY54145) and MTL-R1B (see AY54146). MTL-R1A is a functional seven
CC transmembrane domain form, and MTL-R1B is a truncated five transmembrane
CC domain. The MTL-R1 proteins are used to identify agonists and antagonists
CC which can be used for treating gastric motility disorders, functional
CC defects, disorders secondary to neurological disorders e.g. scleroderma,
CC paraneoplastic syndromes radiation induced dysmotility, diabetes,
CC infections, stress-related motility disorders, psychogenic disorders,
CC gastroparesis, gastro-oesophageal reflux disease, constipation, chronic
CC idiopathic pseudo obstruction, acute faecal impaction, postoperative
CC ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer
CC dyspepsion, non-cardiac chest pain and diarrhoea. They can also be used
CC in the preparation for colonoscopy, endoscopy and duodenal intubation
XX in the preparation for colonoscopy, endoscopy and duodenal intubation
SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;
Query Match 100.0%; Score 1239; DB 3; Length 1239;
Best Local Similarity 100.0%; Pred. No. 3e-215;
Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGAGCCCTGGAAACGGACAGCGGCGCCGAGGGGGCGCGGAGCCCGCTGGGCC 60
DB 1 ATGGGAGCCCTGGAAACGGACAGCGGCGCCGAGGGGGCGCGGAGCCCGCTGGGCC 60
QY 61 GCGCTGCGCCCTTGGAGAGCGCCGCTGCTGCGCCCTTTCCCTCGGGGCGCTGGTGGCG 120
DB 61 GCGCTGCGCCCTTGGAGAGCGCCGCTGCTGCGCCCTTTCCCTCGGGGCGCTGGTGGCG 120
QY 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 ATGCTGATCGGGCGCTACCGGACATGCGGACACACCACTTGTACTTGGGACGATG 240
DB 181 ATGCTGATCGGGCGCTACCGGACATGCGGACACACCACTTGTACTTGGGACGATG 240
QY 241 GCGGTGTCGACCTACTCATCTGCTCGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 GCGGTGTCGACCTACTCATCTGCTCGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 TCGCGGCCCTGGGTGTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 TCGCGGCCCTGGGTGTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 TCGACCTAGCCACGCTGTGACATGACATGACCGGCTCAGGCTGAGCGCTACTTGGCCATC 420
DB 361 TCGACCTAGCCACGCTGTGACATGACATGACCGGCTCAGGCTGAGCGCTACTTGGCCATC 420
QY 421 TCGCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 TCGCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 GTGCTCTGGGCGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 GTGCTCTGGGCGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 CAGGACCCCGGATCTCGTAGTTCGGGCGCTCAATGGACCGCGCGGATCGCTCTCTCG 600
DB 541 CAGGACCCCGGATCTCGTAGTTCGGGCGCTCAATGGACCGCGCGGATCGCTCTCTCG 600
QY 601 CCTCTCGCTCGTCCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 601 CCTCTCGCTCGTCCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 GGGCCCGAGACCGCGAGGCGCGGCGCTGTTTACGCCCGAATGCCGCGAGCCCGCG 720

DB 661 GGGCCCGAGACCGCGAGGCGCGGCGCTGTTTACGCCCGAATGCCGCGAGCCCGCG 720
QY 721 CAGTGGGCGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 CAGTGGGCGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 CTGTGCTTCAGCATCTCTACGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCGCG 840
DB 781 CTGTGCTTCAGCATCTCTACGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGCGCGCG 840
QY 841 CTGCGAGCCCGCGCGCTCGGGCGGAGAGGCGCACCGGCGAGCGTCCGCGTCTCG 900
DB 841 CTGCGAGCCCGCGCGCTCGGGCGGAGAGGCGCACCGGCGAGCGTCCGCGTCTCG 900
QY 901 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 TACATAAACCGAGGATTCGCGGATGATGCTTCTCTCAGTACTTAAACATCGTCTGCT 1020
DB 961 TACATAAACCGAGGATTCGCGGATGATGCTTCTCTCAGTACTTAAACATCGTCTGCT 1020
QY 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTTACAACTCATTTCAAAG 1080
DB 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTTACAACTCATTTCAAAG 1080
QY 1081 AAGTACAGAGCGCGCGCTTTAAACTGCTGCTCGCAAGGAGTCCAGGCCGAGAGGCTTC 1140
DB 1081 AAGTACAGAGCGCGCGCTTTAAACTGCTGCTCGCAAGGAGTCCAGGCCGAGAGGCTTC 1140
QY 1141 CACAGAGCAGGACACCTGCGGGGAAAGTTTCAGGGGACACTGGAGGAGACACGCTGGGC 1200
DB 1141 CACAGAGCAGGACACCTGCGGGGAAAGTTTCAGGGGACACTGGAGGAGACACGCTGGGC 1200
QY 1201 TACACCGAGACAAAGCGCTAACGTAAGACGATGGGATAA 1239
DB 1201 TACACCGAGACAAAGCGCTAACGTAAGACGATGGGATAA 1239
RESULT 2
AAF85449 standard; cDNA; 1239 BP.
XX AAF85449;
AC AAF85449;
XX 23-JUL-2001 (first entry)
DE Nucleotide sequence of a human motilin receptor polypeptide.
XX Motilin receptor; gastrointestinal disease; gastric motility disorder;
KW gastroparesis; irritable bowel syndrome; diarrhoea; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT CDS 1. 1239
FT /tag= a
FT /note= "motilin receptor"
XX WO200132710-A1.
XX 10-MAY-2001.
XX 25-OCT-2000; 2000WO-US029426.
XX 29-OCT-1999; 99US-0162264P.
XX (MERI) MERCK & CO INC.
XX Tan C, McKee K;
XX WPI; 2001-343479/36.

DR P-PSDB: AAB62652.

Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsiq33 polypeptide.

PS Disclosure; Page 102-104; 111pp; English. English.

The invention relates to a method of forming a reversible peptide-receptor complex that involves providing an immobilized receptor, and contacting the receptor with a zsig33 peptide (comprising residues 24-37 of AAB62649), where the receptor binds to the zsig33 peptide. The method is useful for purifying cells, purifying a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, gastric contractility, nutrient uptake, secretion of digestive and pancreatic enzymes and hormones, secretion of insulin-like growth factor -I, secretion of non-zsig33 proteins. It is useful for modulating growth hormone secretion in a mammal having a disease associated with abnormal levels of growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, skeletal dysplasia, immune suppression, obesity, growth retardation, protein catabolic responses after surgery, cachexia, protein loss, dwarfism, wound healing and ovulation induction, treating a mammal having a metabolic disorder requiring neurological feedback, such as satiety regulation, glucose absorption and metabolism and neuropathy-associated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the DNA encoding the long form of motilin receptor, GRF-38A (one of the two isoforms of GPR38 which result from alternative splicing). GPR38 has homology to the human G-protein coupled receptor, GHS-R

Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match
100.0%; Score 1239; ~ DB 4; Length 1239;

Query Match 100.0%; Score 1239; ~ DB 4

Best Local Similarity 100.0%, Freq. NO: 38-213,
Matches 1239: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

[illegible]

PN WO200257791-A2.
XX 25-JUL-2002.
XX 29-NOV-2001; 2001WO-US045219.
XX 29-NOV-2000; 2000US-0250251P.
XX 30-NOV-2000; 2000US-0250452P.
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX Brown JP, Burmer GC, Roush CL, Kulander BG;
XX WPI; 2002-566812/60.
XX P-PSDB; ABG30936.
XX Assay for detecting Alzheimer's disease, Parkinson's disease, ulcerative
XX colitis, Crohn's disease, Hodgkin's disease, glioblastoma or carcinoma,
XX comprises using a binding partner for G protein coupled receptor 38.
XX Disclosure; Fig 1; 112pp; English.
XX The present invention relates to a new assay method that involves
XX contacting a binding partner specific for G protein coupled receptor
XX (GPR) 38 with specific cells. The method of the invention is useful for
XX the detection of an increased risk of Alzheimer's disease, Parkinson's
XX disease, ulcerative colitis, Crohn's disease, Hodgkin's disease,
XX glioblastoma, or carcinoma. GPR 38 is used to manufacture a medicament
XX for inhibiting, treating or preventing Alzheimer's disease, Parkinson's
XX disease, ulcerative colitis, Crohn's disease, Hodgkin's disease,
XX glioblastoma, breast carcinoma, colon carcinoma, lung small cell
XX carcinoma, lung adenocarcinoma, pancreatic small cell carcinoma, and
XX pancreatic adenocarcinoma. An agonist or antagonist to GPR 38 are used to
XX manufacture a medicament able to reduce the symptoms of these diseases.
XX Nucleic acids encoding GPR 38 can also be used to treat the diseases. The
XX present nucleic acid sequence encodes the human G protein- coupled
XX receptor 38 (GPR38) of the invention
XX Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1239; DB 6; Length 1239;
XX Best Local Similarity 100.0%; Pred. No. 3e-215;
XX Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGGGACAGCCCTGGAAACGGACGACCGCCCGGAGGGGGCGCGGAGCGCGCGTGGGCC 60
XX 1 ATGGGACAGCCCTGGAAACGGACGACCGCCCGGAGGGGGCGCGGAGCGCGCGTGGGCC 60
XX
XX 61 GCGCTGCGCGCTTGGACGAGCGCGCTGCTCGCCCTTTTCCCTGGGGCGCGTGTGCGG 120
XX 61 GCGCTGCGCGCTTGGACGAGCGCGCTGCTCGCCCTTTTCCCTGGGGCGCGTGTGCGG 120
XX
XX 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
XX 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
XX
XX 181 ATGCTGATCGGGCGCTACCGGACATGGCGACACACCACTTCTACTTGGGACGATG 240
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XX
XX 241 GCGGTGCGGACCTACTCATCTGCTGGGGTGGCGGTGCGGCTTACCGCTTGTGGCG 300
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XX 301 TCGCGGCGCTGGGTGTTGGGCGCGTGTCTGCGCGCGTGTCTGCTGCTGCTGCTGCTGCTG 360
XX 301 TCGCGGCGCTGGGTGTTGGGCGCGTGTCTGCGCGCGTGTCTGCTGCTGCTGCTGCTGCTG 360
XX
XX 361 TGCACCTAGCCACGCTGTGTCACATGACCGGGCTCAGCGTGGCGGTACTTGGCCATC 420
XX 361 TGCACCTAGCCACGCTGTGTCACATGACCGGGCTCAGCGTGGCGGTACTTGGCCATC 420
XX
XX 421 TGCAGCCCGCTCCGCGCGCGCGTCTTGTGTTACCCGCGCGCGCTCCGCGCGCTCATCGCT 480

Db 421 TGCAGCCCGCTCCGCGCGCGCGTCTTGTGTTACCCGCGCGCGTCCGCGCGCTCATCGCT 480
Qy 481 GTGCTCTGGGCGGTGGCGCTGCTCTCTGCGCGTCCCTTCTTGTCTCTGTTGGGCGCTCGAG 540
Db 481 GTGCTCTGGGCGGTGGCGCTGCTCTCTGCGCGTCCCTTCTTGTCTCTGTTGGGCGCTCGAG 540
Qy 541 CAGGACCCCGGACATCTCCGTAGTCCCGGCGCTCAATGACACCGCGCGGATCGCTTCCTCG 600
Db 541 CAGGACCCCGGACATCTCCGTAGTCCCGGCGCTCAATGACACCGCGCGGATCGCTTCCTCG 600
Qy 601 CCTCTCGGCTGTGCGCGCTCTCTGCGCTCTGCGGGGCGCACCGCGCTCCCGCGCGCTCG 660
Db 601 CCTCTCGGCTGTGCGCGCTCTCTGCGCTCTGCGGGGCGCACCGCGCTCCCGCGCGCTCG 660
Qy 661 GGGCCCGAGACCGGGGAGCGCGCGCTGTTCAGCCCGGAATGCGGCGCGAGCCCGCGG 720
Db 661 GGGCCCGAGACCGGGGAGCGCGCGCTGTTCAGCCCGGAATGCGGCGCGAGCCCGCGG 720
Qy 721 CAGCTGGGCGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 780
Db 721 CAGCTGGGCGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 780
Qy 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGCTGTGAGGAGCGCGCGCGG 840
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGCTGTGAGGAGCGCGCGCGG 840
Qy 841 CTGCGAGCCCGCGCGCTCCGGGCGGAGAGAGCCACCGGACCGCTCCGCGCTCTG 900
Db 841 CTGCGAGCCCGCGCGCTCCGGGCGGAGAGAGCCACCGGACCGCTCCGCGCTCTG 900
Qy 901 CTGTGTGTGTCTGGCATTTTATAATTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 960
Db 901 CTGTGTGTGTCTGGCATTTTATAATTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 960
Qy 961 TACATAACACGGAAGATTCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Db 961 TACATAACACGGAAGATTCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Qy 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCATTTCAAG 1080
Db 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCATTTCAAG 1080
Qy 1081 AAGTACAGAGCGCGCGCTTTAAACTGCTGTGCTGCAAGGAAGTCCAGGCCGAGAGGCTTC 1140
Db 1081 AAGTACAGAGCGCGCGCTTTAAACTGCTGTGCTGCAAGGAAGTCCAGGCCGAGAGGCTTC 1140
Qy 1141 CACAGACGAGGACATGCGGGGAGTTCAGGGGACACTGAGGAGACACGCTGGG 1200
Db 1141 CACAGACGAGGACATGCGGGGAGTTCAGGGGAGTTCAGGGGAGACACGCTGGG 1200
Qy 1201 TACACCGAGACAGCGCTAACGTGAAGACGATGGGATAA 1239
Db 1201 TACACCGAGACAGCGCTAACGTGAAGACGATGGGATAA 1239
XX
XX RESULT 5
XX ID ABZ42842 standard; DNA; 1239 BP.
XX AC ABZ42842;
XX XX
XX DT 04-MAR-2003 (first entry)
XX XX
XX DE Human motilin receptor GPR38 nucleotide SEQ ID NO:472.
XX XX
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX KW G protein-coupled receptor modulator; antibody; immune-related disease;
XX KW growth-related disease; cell regenerative-related disease; AIDS; cancer;
XX KW immunological-related cell proliferative disease; autoimmune disease;
XX KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; ds.
 XX Homo sapiens.
 OS
 XX
 XX WO200261087-A2.
 PN
 XX
 XX 08-AUG-2002.
 PD
 XX
 XX 19-DEC-2001; 2001WO-US050107.
 PF
 XX
 XX 19-DEC-2000; 2000US-0257144P.
 PR
 XX
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA
 XX
 XX Burner GC, Roush CL, Brown JP;
 PI
 XX
 XX WPI: 2003-046718/04.
 DR P-PSDB; ABP81993.
 DR
 XX
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 PT
 XX
 XX Disclosure; Fig 1; 523pp; English.
 PS
 XX
 XX The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42859 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match 100.0%; Score 1239; DB 8; Length 1239;

Best Local Similarity 100.0%; Pred. No. 3e-215;

Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGGAGAGCCCTTGGAAAGCGAGCGAGCGCCCGCGGGGGCGCGGAGCGCGCGTGGCC	60
DB	1	ATGGGAGAGCCCTTGGAAAGCGAGCGAGCGCCCGCGGGGGCGCGGAGCGCGCGTGGCC	60
QY	61	GCCTGCGCCCTTGGAGAGCGAGCGCGCTGCTGCTGCTTCCCTTGGGGCGCTGGTGGCG	120
DB	61	GCCTGCGCCCTTGGAGAGCGAGCGCGCTGCTGCTGCTTCCCTTGGGGCGCTGGTGGCG	120
QY	121	GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180
DB	121	GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180

QY	181	ATGCTGATCGGGCGCTACCGGGAATGCGGACCAACCAACTTGTACCTGGGAGCATG	240
DB	181	ATGCTGATCGGGCGCTACCGGGAATGCGGACCAACCAACTTGTACCTGGGAGCATG	240
QY	241	GCCGTGTCGACCTACTACTCTGCTGCGGTCGGTTCGACCTGACCGGCTCTGGCGC	300
DB	241	GCCGTGTCGACCTACTACTCTGCTGCGGTCGGTTCGACCTGACCGGCTCTGGCGC	300
QY	301	TCGCGGCGCTGGGTGTTTCGGGCGCTGCTGCTGCGCGCTGTCCCTCTACCTGGGAGGGC	360
DB	301	TCGCGGCGCTGGGTGTTTCGGGCGCTGCTGCTGCGCGCTGTCCCTCTACCTGGGAGGGC	360
QY	361	TGCACCTAGCCACGCTGCTGCAATGACCGCGCTCAGCGTGCAGCGCTACCTGGCCATC	420
DB	361	TGCACCTAGCCACGCTGCTGCAATGACCGCGCTCAGCGTGCAGCGCTACCTGGCCATC	420
QY	421	TGCGCGCGCTGCGGCGCGCTGCTGCTGCGCGCTGTCCCTCTACCTGGGAGGGC	480
DB	421	TGCGCGCGCTGCGGCGCGCTGCTGCTGCGCGCTGTCCCTCTACCTGGGAGGGC	480
QY	481	GTGCTCTGGGCGCTGGCGCTGCTGCTGCGCGCTGTCCCTCTGCTGGTGGGCGTGGAG	540
DB	481	GTGCTCTGGGCGCTGGCGCTGCTGCTGCGCGCTGTCCCTCTGCTGGTGGGCGTGGAG	540
QY	541	CAGGACCCCGGCATCTCCGTAGTCCCGGCTCAATGCGACCCGCGGAGCGCTCTCTCG	600
DB	541	CAGGACCCCGGCATCTCCGTAGTCCCGGCTCAATGCGACCCGCGGAGCGCTCTCTCG	600
QY	601	CCTCTGCGCTGCTGCGCGCTGCTGCTGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT	660
DB	601	CCTCTGCGCTGCTGCGCGCTGCTGCTGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT	660
QY	661	GGGCGCAGAGCCGCGGAGCGCGCTGCTGCTGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCT	720
DB	661	GGGCGCAGAGCCGCGGAGCGCGCTGCTGCTGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCT	720
QY	721	CAGTGGGCGCGCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	780
DB	721	CAGTGGGCGCGCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	780
QY	781	CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGCTGTGGAGCAGCGCGCGCGCG	840
DB	781	CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGCTGTGGAGCAGCGCGCGCGCGCG	840
QY	841	CTGCGAGCGCGCGCGCTCGGGGCGGAGAGGCGCACCGGCGAGCGCTCGCGTCTCTG	900
DB	841	CTGCGAGCGCGCGCGCTCGGGGCGGAGAGGCGCACCGGCGAGCGCTCGCGTCTCTG	900
QY	901	CTGTGCTGCTGCGCATTTTATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	960
DB	901	CTGTGCTGCTGCGCATTTTATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	960
QY	961	TACATAACAGGAGATTCGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1020
DB	961	TACATAACAGGAGATTCGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1020
QY	1021	CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCAATTTCAAG	1080
DB	1021	CTGCAACTTTTCTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCAATTTCAAG	1080
QY	1081	AAGTACAGAGCGGCGCTTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
DB	1081	AAGTACAGAGCGGCGCTTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
QY	1141	CACAGAGCGGAGCATTCGGGGGAGCTTCGCGGAGCTGTGGAGGAGACACGCTGGGC	1200
DB	1141	CACAGAGCGGAGCATTCGGGGGAGCTTCGCGGAGCTGTGGAGGAGACACGCTGGGC	1200
QY	1201	TACACCGGAGCAAGCGCTTAAAGTGAAGACGATGGGATAA	1239
DB	1201	TACACCGGAGCAAGCGCTTAAAGTGAAGACGATGGGATAA	1239

RESULT 6	
ADN11760	
ID	ADN11760 standard; cDNA; 1239 BP.
XX	
AC	ADN11760;
XX	
DT	15-JUL-2004 (first entry)
XX	
DE	Human motilin receptor GPR-38A coding sequence.
XX	
ss	gene; human; zsig33; body weight; body mass; antibody; antagonist;
KW	gastrointestinal; antiinflammatory; antiulcer; vulnerary;
KW	growth hormone secretagogue; GHS-R; peptide-antibody complex;
KW	motilin receptor.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..1239
FT	/*tag= a
FT	/product= "motilin receptor GPR38A"
XX	
PN	WO2004033645-A2.
XX	
PD	22-APR-2004.
XX	
PP	06-OCT-2003; 2003WO-US031804.
PR	
PR	07-OCT-2002; 2002US-0416918P.
XX	
PA	(Zymo) ZYMOGENETICS INC.
XX	
PI	Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;
XX	
DR	WPI; 2004-340913/31.
XX	
DR	P-PSDB; ADN11761.
XX	
PT	Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,
PT	inhibiting signal transduction in a cell expressing a growth hormone
PT	secretagogue receptor, or treating a metabolic disorder.
XX	
PS	Disclosure; Page 94-95; 100pp; English.
XX	
CC	The present invention relates to the use of a zsig33 peptide for forming
CC	a peptide-antibody complex, purifying a peptide, inhibiting signal
CC	transduction in a cell expressing a growth hormone secretagogue receptor
CC	(GHS-R), decreasing fat deposition in a mammal, suppressing the appetite
CC	of a mammal, inhibiting growth hormone secretion in pituitary cells of a
CC	mammal, or treating a metabolic disorder. The peptide is useful for
CC	forming a peptide-antibody complex, purifying a peptide, inhibiting
CC	signal transduction in a cell expressing a GHS-R, decreasing fat
CC	deposition in a mammal, suppressing the appetite of a mammal, inhibiting
CC	growth hormone secretion in pituitary cells of a mammal, or treating a
CC	metabolic disorder. The zsig33 polypeptides can be used to study
CC	proliferation or differentiation in stomach, lung, pituitary,
CC	hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,
CC	skeletal muscle or pancreas. They are also useful in delivering
CC	therapeutic agents. Zsig33 polypeptides, agonists and antagonists are
CC	also useful for promoting wound healing. The polypeptides, nucleic acids
CC	and antibodies are useful for diagnosing, treating or preventing
CC	disorders associated with gastric reflux, gastroparesis, modulation of
CC	secretion of pituitary hormones, including growth hormone, Crohn's
CC	disease, metabolic wasting, gastric ulcers, weight management, or
CC	degenerative disease. The present sequence is the human motilin receptor
CC	GPR38A coding sequence shown in the exemplification of the invention.
XX	
SQ	Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1239; DB 12; Length 1239;
	Best Local Similarity 100.0%; Pred. No. 3e-215;
	Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATGGGACGCCCTGGAAACGGCAGCGCGCCCGAGGGGGCGCGGAGCCCGCGTGGCCCC 60

Db 1081 AAGTACAGACGGCGCGCTTTAAACTGCTGCTCGAAGGAAGTCCAGGCCGAGAGGCTTC 1140
 Qy 1141 CACAGAAGCAGGACACTCGCGGGGAGTTGACAGGGACACTGGAGGACACGCTGGGC 1200
 Db 1141 CACAGAAGCAGGACACTCGCGGGGAGTTGACAGGGACACTGGAGGACACGCTGGGC 1200
 Qy 1201 TACACCGAGACAAGCGCTTAACGTGAAGACGATGGGATAA 1239
 Db 1201 TACACCGAGACAAGCGCTTAACGTGAAGACGATGGGATAA 1239

RESULT 7

AD030072

ID AD030072 standard; cDNA; 1239 BP.

XX

AC AD030072;

DT 29-JUL-2004 (first entry)

XX

DE Human GPCR GPR38 polynucleotide, SEQ ID NO:1174.

XX

KW G protein-coupled receptor; GPCR; drug screening; diagnosis;

KW transgenic mouse; neurological disorder; adrenal gland disorder;

KW colon disorder; intestinal disorder; cardiovascular disorder;

KW muscular disorder; blood disorder; immune disorder; bone disorder;

KW joint disorder; metabolic disorder; nutritive disorder; cancer;

KW kidney disorder; liver disorder; lung disorder; breast disorder;

KW ovary disorder; uterus disorder; prostate disorder; testis disorder;

KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;

KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;

KW cytotatic; antinflammatory; vasotropic; antiangiinal; antiarrhythmic;

KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;

KW viricide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;

KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;

KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;

KW Gene; ss.

XX

OS Homo sapiens.

XX

PN WO2004040000-A2.

XX

PD 13-MAY-2004.

XX

PF 09-SEP-2003; 2003WO-US028226.

XX

PR 09-SEP-2002; 2002US-0409103P.

XX

PR 09-APR-2003; 2003US-0461329P.

XX

PA (PRIM-) PRIMAL INC.

XX

PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;

XX

XX WPI; 2004-390329/36.

XX

DR P-PSDB; ADO29697.

XX

PT Novel mammalian G protein coupled receptors, useful for identifying

PT compounds that modulates diagnosing and treating disease condition

PT associated with GPCR dysfunction e.g. autoimmune diseases, angina

PT pectoris, Parkinson's disease.

XX

PS Claim 151; SEQ ID NO 1174; 542pp; English.

XX

CC The invention relates to human and mouse G protein-coupled receptors

CC (GPCRs) and nucleic acids encoding them. The invention also relates to

CC sequences at least 90% identical to the GPCR proteins and nucleic acids

CC of the invention; methods of treating, preventing or diagnosing diseases

CC associated with GPCRs of the invention; methods of screening for

CC compounds useful in the treatment of GPCR-related diseases; a transgenic

CC mouse comprising a GPCR gene of the invention; a mouse comprising a

CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived

CC from the transgenic mice; kits comprising several mice, each of which has

CC a mutation in a different GPCR gene of the invention; and kits comprising

CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
 CC nucleic acid of the invention. Note: The full sequence data for this
 CC patent did not form part of the printed specification; those sequences
 CC not shown were obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

XX

Query Match 100.0%; Score 1239; DB 12; Length 1239;

XX

Best Local Similarity 100.0%; Pred. No. 3e-215;

XX

Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 ATGGGCGACCCCTTGAACGGCAGCAGCGCCCCGAGGGGGCGCGGAGCCCGCTGGGCC 60

Db 1 ATGGGCGACCCCTTGAACGGCAGCAGCGCCCCGAGGGGGCGCGGAGCCCGCTGGGCC 60

XX

Qy 61 GCGCTGCGCCCTCGGACGAGCGCGCTGCTGCGCCCTTCCCTGGGGGGCGCTGGTGGCG 120

Db 61 GCGCTGCGCCCTCGGACGAGCGCGCTGCTGCGCCCTTCCCTGGGGGGCGCTGGTGGCG 120

XX

Qy 121 GTGACCGCTGTGTGCTGTGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180

Db 121 GTGACCGCTGTGTGCTGTGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180

XX

Qy 181 ATGCTGATCGGGCGCTACCGGGACATGGGACACACACCACTTGTACCTGGGAGCATG 240

Db 181 ATGCTGATCGGGCGCTACCGGGACATGGGACACACCACTTGTACCTGGGAGCATG 240

XX

Qy 241 GCGGTGTCGACCTACTCATCTCTCGGGCTGCGCTTTCGACCTGTACCGCTCTGGGGC 300

Db 241 GCGGTGTCGACCTACTCATCTCTCGGGCTGCGCTTTCGACCTGTACCGCTCTGGGGC 300

XX

Qy 301 TCGCGGGCCCTGGGTGTTGGGGCGCTGCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

Db 301 TCGCGGGCCCTGGGTGTTGGGGCGCTGCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

XX

Qy 361 TGCACCTACGCCACGCTGTGCACATGACCGCGCTACGCTGCGAGCGCTACCTGGCCATC 420

Db 361 TGCACCTACGCCACGCTGTGCACATGACCGCGCTACGCTGCGAGCGCTACCTGGCCATC 420

XX

Qy 421 TGCAGCGCGCTTCGCGCCCGGCTCTTGTGTACCCCGCGCGCGCTTCGCGCGCTCATCGCT 480

Db 421 TGCAGCGCGCTTCGCGCCCGGCTCTTGTGTACCCCGCGCGCGCTTCGCGCGCTCATCGCT 480

XX

Qy 481 GTGCTGTGGGCGGTGGGGCTGCTCTCTGCGGGTCCCTTCTTGTTCCTGTGGGGGTGAG 540

Db 481 GTGCTGTGGGCGGTGGGGCTGCTCTCTGCGGGTCCCTTCTTGTTCCTGTGGGGGTGAG 540

XX

Qy 541 CAGACCCCGGCATCTCGGTAGTCCCGGGCTCAATGGCACCGCGCGGATCGCTCTCTCG 600

Db 541 CAGACCCCGGCATCTCGGTAGTCCCGGGCTCAATGGCACCGCGCGGATCGCTCTCTCG 600

XX

Qy 601 CCTCTCGCTCTGTGCGCGCTCTCTGTGCTCTCGGGGGCGCCACCGCGCTCCCCCGCGCTG 660

Db 601 CCTCTCGCTCTGTGCGCGCTCTCTGTGCTCTCGGGGGCGCCACCGCGCTCCCCCGCGCTG 660

XX

Qy 661 GGGCCCGAGACCGCGGAGGGCGGCGCTGTTCAGCGCGGATGCGGGCGAGCCCCGCG 720

Db 661 GGGCCGAGACCGCGGCGCGCTGTTACCGCGAATCGCGCGAGCCCGCG 720
Qy 721 CAGCTGGGCGCGCTCGGTGTATGCTGTGGGTGACACCGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGGCGCGCTCGGTGTATGCTGTGGGTGACACCGCTACTTCTTCTGCGCTTT 780
Qy 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGTGTGAGCAGCGCGGCGG 840
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGTGTGAGCAGCGCGGCGG 840
Qy 841 CTGCGAGCGCGCGCTCGGGCGGAGGAGCGACCGGACCGTCCGGTCTG 900
Db 841 CTGCGAGCGCGCGCTCGGGCGGAGGAGCGACCGGACCGTCCGGTCTG 900
Qy 901 CTGTGTGGTGTCTGGCATTTATAATTTGCTGTGGTCCCTTCCAGTTGGCAGATCAAT 960
Db 901 CTGTGTGGTGTCTGGCATTTATAATTTGCTGTGGTCCCTTCCAGTTGGCAGATCAAT 960
Qy 961 TACATAAACACGGAAGATTCGGGATGATGTAATCTCTCAGTACTTTAAATCGTCT 1020
Db 961 TACATAAACACGGAAGATTCGGGATGATGTAATCTCTCAGTACTTTAAATCGTCT 1020
Qy 1021 CTGCAACTTTCTATCTGAGCGCATCTATCAACCAATCCTTACAACTCAATTTCAAG 1080
Db 1021 CTGCAACTTTCTATCTGAGCGCATCTATCAACCAATCCTTACAACTCAATTTCAAG 1080
Qy 1081 AAGTACAGACGGCGCTTTAAATCTGCTGCTGCAAGGAGTCCAGGCCGAGAGGCTTC 1140
Db 1081 AAGTACAGACGGCGCTTTAAATCTGCTGCTGCAAGGAGTCCAGGCCGAGAGGCTTC 1140
Qy 1141 CACAGAAGCAGGACACTCGCGGGAAGTTGACGGGACACTGGAGGAGACACGTTGGC 1200
Db 1141 CACAGAAGCAGGACACTCGCGGGAAGTTGACGGGACACTGGAGGAGACACGTTGGC 1200
Qy 1201 TACACCGAGACAGCGCTTAACGTGAAGACGATGGGATAA 1239
Db 1201 TACACCGAGACAGCGCTTAACGTGAAGACGATGGGATAA 1239
RESULT 8
ADQ37920
ID ADQ37920 standard; DNA; 1239 BP.
XX
AC ADQ37920;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human G-protein-coupled receptor 38 coding sequence.
XX
KW ds; gene; antiparkinsonian; neuroprotective; nootropic; cardiovascular;
KW cardiant; vasotropic; antiarteriosclerotic; nephrotropic; utroptic;
KW urology disease; cardiovascular disease;
KW peripheral nervous system disorder; central nervous system disorder;
KW G-protein-coupled receptor 38; GPR38; Parkinson's disease;
KW multiple sclerosis; dementia; myocardial infarction; ischemic disease;
KW atherosclerosis; renal failure; glomerulopathy; urinary incontinence.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1239
FT FT /*tag= a
FT FT /product= "G-coupled receptor protein 38"
XX
FN WO2004057328-A2.
XX
PD 08-JUL-2004.
XX
PF 11-DEC-2003; 2003WO-EP014052.
XX
PR 23-DEC-2002; 2002EP-00028753.
XX

(FARB) BAYER HEALTHCARE AG.
Golz S, Brueggemeier U, Summer H;
WPI; 2004-543310/52.
P-P8DB; ADQ37921.
Screening therapeutic agents for use in treatment of urology diseases and cardiovascular diseases in a mammal, comprises contacting a test compound with G-protein-coupled receptor 38, and detecting binding.
Disclosure; SEQ ID NO 1; 111pp; English.
The invention relates to a method of screening (M1) for therapeutic agents useful in the treatment of a disease chosen from urology diseases, cardiovascular diseases and disorders of the peripheral and central nervous system in a mammal, comprises contacting a test compound with a G-protein-coupled receptor 38 (GPR38) polypeptide, and detecting binding of the test compound to the GPR38 polypeptide. (M1) is useful for screening therapeutic agents useful in the treatment of a disease chosen from urology diseases, cardiovascular diseases and disorders of the peripheral and central nervous system in a mammal, such as Parkinson's disease, multiple sclerosis, dementia, cardiovascular disorders such as myocardial infarction, ischemic diseases, atherosclerosis, and urological disorders such as acute or chronic renal failure, glomerulopathies, and urinary incontinence. This sequence corresponds to the nucleic acid encoding the human G-protein-coupled receptor 38.
Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;
Query Match 100.0%; Score 1239; DB 12; Length 1239;
Best Local Similarity 100.0%; Pred. No. 3e-215;
Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGGCGAGCCCTCGAAGCGGAGCGCGCCCGGAGGCGCGGAGCGCGGCGGCGG 60
Db 1 ATGGGCGAGCCCTCGAAGCGGAGCGCGCCCGGAGGCGCGGAGCGCGGCGGCGG 60
Qy 61 GCGCTGCGCGCTTGGGAGCGCGCGCTGCTGCGCCCTTTTCCCGGCGCGCTGCGCG 120
Db 61 GCGCTGCGCGCTTGGGAGCGCGCGCTGCTGCGCCCTTTTCCCGGCGCGCTGCGCG 120
Qy 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 180
Db 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 180
Qy 181 ATGCTGATCGGGCGCTACCGGAGCATCGGAGCACCAACCACTTGTACTCGGAGCATG 240
Db 181 ATGCTGATCGGGCGCTACCGGAGCATCGGAGCACCAACCACTTGTACTCGGAGCATG 240
Qy 241 GCCGTGTCGACCTACTCATCTGCTCGGGCTGCGCTTTCGACCTGTACCGCTCTGGGCG 300
Db 241 GCCGTGTCGACCTACTCATCTGCTCGGGCTGCGCTTTCGACCTGTACCGCTCTGGGCG 300
Qy 301 TCGCGGCGCTCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 360
Db 301 TCGCGGCGCTCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 360
Qy 361 TGCACCTACGCGAGCTGCTGACATGACCGGCTGACGCGTCTGCTGCTGCTGCTGCTG 420
Db 361 TGCACCTACGCGAGCTGCTGACATGACCGGCTGACGCGTCTGCTGCTGCTGCTGCTG 420
Qy 421 TCGCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 TCGCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 GTGCTCTGGGCGGTGGGCGTCTCTCTGCGCGTCCCTTCTTCTTCTTCTTCTTCTTCTG 540
Db 481 GTGCTCTGGGCGGTGGGCGTCTCTCTGCGCGTCCCTTCTTCTTCTTCTTCTTCTTCTG 540
Qy 541 CAGGACCGCGCATCTCGGTAGTCCCGGCGCTCAATGGCACCGCGCGATCGCTCTCTCG 600
Db 541 CAGGACCGCGCATCTCGGTAGTCCCGGCGCTCAATGGCACCGCGCGATCGCTCTCTCG 600

QY 601 CCTCTCGCTCGTCCGCGCTCTCTGGCTCTCGCGGCGCCACCGCGTCCCGCGCGTCCG 660
 DB |||||
 QY 601 CCTCTCGCTCGTCCGCGCTCTCTGGCTCTCGCGGCGCCACCGCGTCCCGCGCGTCCG 660
 DB |||||
 QY 661 GGGCCCGAGACCGCGAGCGCGCGCTGTTTCAGCCGCGAATGCGCGCGAGCCCGCG 720
 DB |||||
 QY 661 GGGCCCGAGACCGCGAGCGCGCGCTGTTTCAGCCGCGAATGCGCGCGAGCCCGCG 720
 DB |||||
 QY 721 CAGTGGGCGCGTGGTGTATGTGTGGGTACACCGCCTACTTCTTCTGCGCCTTT 780
 DB |||||
 QY 721 CAGTGGGCGCGTGGTGTATGTGTGGGTACACCGCCTACTTCTTCTGCGCCTTT 780
 DB |||||
 QY 781 CTGTGCTCAGCATCTCTACCGGCTCATCGGCGCGGAGCTGTGAGACGCGCGCG 840
 DB |||||
 QY 781 CTGTGCTCAGCATCTCTACCGGCTCATCGGCGCGGAGCTGTGAGACGCGCGCG 840
 DB |||||
 QY 841 CTGCGAGCGCGCGCTCTCGGCGGAGAGAGCCACCGCGAGACCGTCCGCGTCTG 900
 DB |||||
 QY 841 CTGCGAGCGCGCGCTCTCGGCGGAGAGAGCCACCGCGAGACCGTCCGCGTCTG 900
 DB |||||
 QY 901 CTGTTGGTGGTCTGGCATTTAATTTGCTGGTGGCTTCCAGTGGGAGAAATCAT 960
 DB |||||
 QY 901 CTGTTGGTGGTCTGGCATTTAATTTGCTGGTGGCTTCCAGTGGGAGAAATCAT 960
 DB |||||
 QY 961 TACATAACACGAGATTCGCGGATGATGTAATCTCTCAGTACTTTAAACATCGTCT 1020
 DB |||||
 QY 961 TACATAACACGAGATTCGCGGATGATGTAATCTCTCAGTACTTTAAACATCGTCT 1020
 DB |||||
 QY 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCCAACTCTCAACCTCATTTCAA 1080
 DB |||||
 QY 1021 CTGCAACTTTTCTATCTGAGCGCATCTATCAACCCAACTCTCAACCTCATTTCAA 1080
 DB |||||
 QY 1081 AGTACAGAGCGCGCTTTAACTGCTGCTCGCAAGAGTCCAGCGCGAGAGCTTC 1140
 DB |||||
 QY 1081 AGTACAGAGCGCGCTTTAACTGCTGCTCGCAAGAGTCCAGCGCGAGAGCTTC 1140
 DB |||||
 QY 1141 CACAGAGCAGGACACTCGCGGGAAGTTGCGGGGACACTGGAGGAGACACGTTGG 1200
 DB |||||
 QY 1141 CACAGAGCAGGACACTCGCGGGAAGTTGCGGGGACACTGGAGGAGACACGTTGG 1200
 DB |||||
 QY 1201 TACACGAGACAAAGCGCTTAACGTGAAGACGATGGGATAA 1239
 DB |||||
 QY 1201 TACACGAGACAAAGCGCTTAACGTGAAGACGATGGGATAA 1239
 DB |||||

RESULT 9

AA166989
 ID AA166989 standard; DNA; 1506 BP.

AC AA166989;

DT 30-JAN-2002 (first entry)

XX Human GPR38 variant GPR38V polypeptide encoding DNA.

KW GPR38V; variant; antibacterial; cytotatic; analgesic; antiaesthetic;
 KW anti-Parkinsonian; hypertensive; hypotensive; antidiabetic; osteopathic;
 KW antiallergic; antimigraine; neuroleptic; nootropic; anticonvulsant;
 KW antiulcer; antiemetic; cardiant; vaccine; ds.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..1506

FT /*tag= a

FT /product= "GPR38V"

XX WO200164836-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006277.

XX

PR 01-MAR-2000; 2000US-00516315.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Elshourbagy N, Shabon U;

XX WPI; 2001-639956/73.

XX P-PSDB; AAG65822.

XX

PT New human GPR38V polypeptide and polynucleotide, useful for treating e.g.
 PT bacterial, fungal, protozoal and viral infections, cancers or allergies,
 PT as vaccines, and for identifying agonists and antagonists potentially
 PT useful in therapy.

PS Claim 2; Page 26; 32pp; English.

XX

CC This DNA encodes a human GPR38 variant (GPR38V) polypeptide. GPR38V can
 CC be expressed by standard recombinant methodology. The polynucleotides and
 CC polypeptides are used in the treatment of bacterial, fungal, protozoal
 CC and viral infections, infections caused by HIV-1 or HIV-2, pain, cancers,
 CC diabetes, obesity, anorexia, asthma, Parkinson's disease, acute heart
 CC failure, hypertension, urinary retentions, osteoporosis, allergies,
 CC ulcers, migraine, psychotic and neurological disorders, or dyskinesias.
 CC They are also useful for identifying agonists and antagonists that are
 CC potentially useful in therapy, as vaccines to induce immunological
 CC response in a mammal. The polypeptides may also be used as immunogens to
 CC produce antibodies immunospecific for the polypeptides, and to identify
 CC membrane bound or soluble receptors

SQ Sequence 1506 BP; 207 A; 534 C; 509 G; 256 T; 0 U; 0 Other;

Query Match 100.0%; Score 1239; DB 4; Length 1506;

Best Local Similarity 100.0%; Pred. No. 3e-215;

Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAGCGCCCTCGAAGCGGAGCGAGCGCGCGCGGCGCGGCGCGCGCGCGCGCGCG 60

DB 268 ATGGGAGCGCCCTCGAAGCGGAGCGAGCGCGCGCGGCGCGGCGCGCGCGCGCGCGCG 327

QY 61 GCGTGGCGCGCTTCGAGCGAGCGCGCTGCTCGCCCTTTCCCTGGGGGGCGCTGGTGGCG 120

DB 328 GCGTGGCGCGCTTCGAGCGAGCGCGCTGCTCGCCCTTTCCCTGGGGGGCGCTGGTGGCG 387

QY 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

DB 388 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447

QY 181 ATGCTGATCGGGCGCTACCGGGACATCGGGACACCAACCACTTGTACCTGGGCGAGCATG 240

DB 448 ATGCTGATCGGGCGCTACCGGGACATCGGGACACCAACCACTTGTACCTGGGCGAGCATG 507

QY 241 GCGTGTCCGACCTACTCATCTCTCGGGCTGCGCTTTCGACCTGTACCGCTCTGGCGC 300

DB 508 GCGTGTCCGACCTACTCATCTCTCGGGCTGCGCTTTCGACCTGTACCGCTCTGGCGC 567

QY 301 TCGGGCGCGCTGGGCTGCGCGCTGCTGCTGCGCGCTGCTGCTGCGCGCTGCGCGCGCG 360

DB 568 TCGGGCGCGCTGGGCTGCGCGCTGCTGCTGCGCGCTGCTGCTGCGCGCTGCGCGCGCG 627

QY 361 TGCACCTACGCGCGCTGCTGACATGACCGCGCTCAGCGCTCAGCGCGCTACCTGGCCATC 420

DB 628 TGCACCTACGCGCGCTGCTGACATGACCGCGCTCAGCGCTCAGCGCGCTACCTGGCCATC 687

QY 421 TCGCGCGCGCTTCGCGCGCGCGCTTGTGTTACCGCGCGCGCGCTTCGCGCGCGCTCATCGCT 480

DB 688 TCGCGCGCGCTTCGCGCGCGCGCTTGTGTTACCGCGCGCGCGCTTCGCGCGCGCTCATCGCT 747

QY 481 GTGCTCTGGGCGCGTGGCGCTGCTCTCTGCGCGCTCCCTTCTTGTCTGCTGGGCGTGGAG 540

DB 748 GTGCTCTGGGCGCGTGGCGCTGCTCTCTGCGCGCTCCCTTCTTGTCTGCTGGGCGTGGAG 807

QY 541 CAGGACCCCGGCACTCTCCGTAGTCCCGGCGCTCAATGGCACCGCGCGAGATCGCCTCTCTCG 600

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Db 808 CAGGACCCCGGATCTCGTAGTCCCGGCCCTCAATGGACCGCGGATCGCCCTCCG 867
Qy 601 CCTCTCGCCTCGTCCGCGCTCTCTGGCTCTCGCGGGGCCACACCGCCGCGCGTCG 660
Db 868 CCTCTCGCCTCGTCCGCGCTCTCTGGCTCTCGCGGGGCCACACCGCGCGTCG 927
Qy 661 GGGCCGAGACCGCGGAGCCGCGCGCTGTTACGCGGGAATGCGCGCGAGCCCGCG 720
Db 928 GGGCCGAGACCGCGGAGCCGCGCGCTGTTACGCGGGAATGCGCGCGAGCCCGCG 987
Qy 721 CAGCTGGGCGCTCGTGTCTATCTGTGGTTCACACCGCTACTCTTCTGCGCCCTT 780
Db 988 CAGCTGGGCGCTCGTGTCTATCTGTGGTTCACACCGCTACTCTTCTGCGCCCTT 1047
Qy 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCGCG 840
Db 1048 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCGCG 1107
Qy 841 CTGCGAGGCCCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCGTCCGCTCTG 900
Db 1108 CTGCGAGGCCCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCGTCCGCTCTG 1167
Qy 901 CTGCTGGTGTCTCGCATTTATATTCTGCTGTTGCCCTTCCAGTTGGCAGATCAT 960
Db 1168 CTGCTGGTGTCTCGCATTTATATTCTGCTGTTGCCCTTCCAGTTGGCAGATCAT 1227
Qy 961 TACATAAACACGGAAGATTCGCGGATGATGTACTTCTCTCAGTACTTTAAACATCTGCT 1020
Db 1228 TACATAAACACGGAAGATTCGCGGATGATGTACTTCTCTCAGTACTTTAAACATCTGCT 1287
Qy 1021 CTGCAACTTTTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCAATTTCAAAG 1080
Db 1288 CTGCAACTTTTATCTGAGCGCATCTATCAACCAATCTCTCAACCTCAATTTCAAAG 1347
Qy 1081 AGTACAGCGCGCGCTTTAACTGCTGCTCGCAAGGAGTCCAGCGCGAGGCTTC 1140
Db 1348 AGTACAGCGCGCGCTTTAACTGCTGCTCGCAAGGAGTCCAGCGCGAGGCTTC 1407
Qy 1141 CACAGAAGCAGGACACTCGCGGGGAAGTTGAGGGGACACTGAGGAGACACAGTGGCG 1200
Db 1408 CACAGAAGCAGGACACTCGCGGGGAAGTTGAGGGGACACTGAGGAGACACAGTGGCG 1467
Qy 1201 TACACCGAGACAAGCGCTAACTGAAGACGATGGGATAA 1239
Db 1468 TACACCGAGACAAGCGCTAACTGAAGACGATGGGATAA 1506

```

RESULT 10

AAZ45404

ID AAZ45404 standard; cdna; 1390 BP.

XX AC AAZ45404;

XX XX

DT 27-MAR-2000 (first entry)

XX DE

cdna encoding the motilin receptor splice variant MTL-R1b.

Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;
 spliced form; MTL-R1a; MTL-R1b; Gastric motility disorder;
 functional defect; neurological disorder; scleroderma; colonoscopy;
 paraneoplastic syndrome; radiation induced dysmotility; diabetes;
 infection; stress-related motility disorder; psychogenic disorder;
 gastroparesis; gastro-oesophageal reflux disease; constipation;
 chronic idiopathic pseudo obstruction; acute faecal impaction;
 postoperative ileus; gallstones; infantile colic; diarrhoea;
 irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;
 endoscopy; duodenal intubation; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FH CDS 1..1161

FT

/*tag= a
 /product= "MTL-R1b"

WO994436-A1.

16-DEC-1999.

08-JUN-1999; 99WO-US012773.

12-JUN-1998; 98US-0089098P.

(MERI) MERCK & CO INC.

Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;

Pong S, Smith EG;

WPI; 2000-105868/09.

P-PSDB; AAY54146.

Novel receptor protein for screening compounds used in treating irritable

bowel syndrome, constipation and other gastric conditions.

Claim 6; Fig 4; 44pp; English.

The present sequence encodes splice variant MTL-R1b of the motilin

receptor. The gene encodes a G-protein coupled receptor, and is

designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1a

(see AAY54145) and MTL-R1b (see AAY54146). MTL-R1a is a functional seven

transmembrane domain form, and MTL-R1b is a truncated five transmembrane

domain. The MTL-R1 proteins are used to identify agonists and antagonists

which can be used for treating gastric motility disorders, functional

defects, disorders secondary to neurological disorders e.g. scleroderma,

paraneoplastic syndromes radiation induced dysmotility, diabetes,

infections, stress-related motility disorders, psychogenic disorders,

gastroparesis, gastro-oesophageal reflux disease, constipation, chronic

idiopathic pseudo obstruction, acute faecal impaction, postoperative

ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer

dyspepsia, non-cardiac chest pain and diarrhoea. They can also be used

in the preparation for colonoscopy, endoscopy and duodenal intubation

SQ Sequence 1390 BP; 190 A; 496 C; 436 G; 268 T; 0 U; 0 Other;

Query Match 87.0%; Score 1078; DB 3; Length 1390;

Best Local Similarity 89.1%; Pred. No. 4.3e-186;

Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

Qy 1 ATGGGACGCCCTTGAACGGCAGCAGCGGCCCGCGGGGGCGCGGAGCGCGCGCGCC 60

Db 1 ATGGGACGCCCTTGAACGGCAGCAGCGGCCCGCGGGGGCGCGGAGCGCGCGCGCC 60

Qy 61 GCGCTGCGCGCTTGGCAGCGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCGTGTGCGG 120

Db 61 GCGCTGCGCGCTTGGCAGCGCGCGCTGCTGCGCCCTTTCCCTGGGGCGCGTGTGCGG 120

Qy 121 GTGACCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

Db 121 GTGACCGCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

Qy 181 ATGCTGATCGGGCGCTACCGGACATCGGACACACCACTTGTACTCGGCGAGCATG 240

Db 181 ATGCTGATCGGGCGCTACCGGACATCGGACACACCACTTGTACTCGGCGAGCATG 240

Qy 241 GCGGTGTCGACCTACTCATCTGCTCGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 300

Db 241 GCGGTGTCGACCTACTCATCTGCTCGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 300

Qy 301 TCGGGCGCTGGGTGTTGCGGCGCGCTGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTG 360

Db 301 TCGGGCGCTGGGTGTTGCGGCGCGCTGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTG 360

Qy 361 TGCACCTACGCGACGCTGCTGCATGACCGCGCTCAGCGCTGAGCGCTACTGCGCCATC 420

Db 361 TGCACCTACGCGACGCTGCTGCATGACCGCGCTCAGCGCTGAGCGCTACTGCGCCATC 420

QY 421 TGCAGCCGCTCCGCGCGCGCTTCTTGGTACCCGCGCGCGCTCCGCGCGCTCATCGCT 480
 Db 421 TGCAGCCGCTCCGCGCGCGCTTCTTGGTACCCGCGCGCGCTCCGCGCGCTCATCGCT 480
 QY 481 GTGCTCTGGCGCGCTGGCGCTCTCTCTGCGGTCCTTCTTCTTCTGTTGGCGCTCGAG 540
 Db 481 GTGCTCTGGCGCGCTGGCGCTCTCTCTGCGGTCCTTCTTCTTCTGTTGGCGCTCGAG 540
 QY 541 CAGGACCCCGGATCTCCGTAATGCTGCGCGGCTCAATGGACCGCGCGGATGCGCTCTCG 600
 Db 541 CAGGACCCCGGATCTCCGTAATGCTGCGCGGCTCAATGGACCGCGCGGATGCGCTCTCG 600
 QY 601 CCTCTGCGCTCTGCGCGGCTCTCTGCGGTCCTTCTTCTGCGGTCCTTCTTCTGCGGTCG 660
 Db 601 CCTCTGCGCTCTGCGCGGCTCTCTGCGGTCCTTCTTCTGCGGTCCTTCTTCTGCGGTCG 660
 QY 661 GGGCCCGAGACCGCGAGCGCGGCTGTTTACGCGGATGCGGCGCGAGCGCGCG 720
 Db 661 GGGCCCGAGACCGCGAGCGCGGCTGTTTACGCGGATGCGGCGCGAGCGCGCG 720
 QY 721 CAGCTGGCGCGCTGGGTCTATGCTGGGTCTACCGGCTCTTCTTCTGCGGCTTT 780
 Db 721 CAGCTGGCGCGCTGGGTCTATGCTGGGTCTACCGGCTCTTCTTCTGCGGCTTT 780
 QY 781 CTGTCCTCAGCATCTCTACCGGCTCATCGGCGGAGCTGTGAGCAGCGCGCGCG 840
 Db 781 CTGTCCTCAGCATCTCTACCGGCTCATCGGCGGAGCTGTGAGCAGCGCGCGCG 840
 QY 841 CTGCGAGCGCGCGCTCTGCGGCGGAGAGAGCGCGCGCGCGCTGCGGCTCTG 900
 Db 841 CTGCGAGCGCGCGCTCTGCGGCGGAGAGAGCGCGCGCGCGCTGCGGCTCTG 900
 QY 901 C----- 901
 Db 901 CGTAAGTGGAGCGCGGTGTTTCAAAGACGCTGCTGCGCGCGCGCGCGGAC 960
 QY 902 ----- 901
 Db 961 GCGCAACGCTGGTGGTCCCTTCTGCTGCGCGAGCTCTGGGCGCGCTCCAGCTCC 1020
 QY 902 -----TGTTGGTGGTCTTGGCATTTATTAATTG 929
 Db 1021 TTTCTTATTTGATTCCAGCTCCACCGCGGTGGTGGTCTTGGCATTTATTAATTG 1080
 QY 930 CTGGTTGCTTCCAGTTGGCAGATCATTTACATAACAGGAGATTCGCGATGAT 989
 Db 1081 CTGGTTGCTTCCAGTTGGCAGATCATTTACATAACAGGAGATTCGCGATGAT 1140
 QY 990 GTACTTCTCTAGTACTTTAAATCATGCTGCTCTGCAACTTTTCTATCTGAGCGCATCTAT 1049
 Db 1141 GTACTTCTCTAGTACTTTAAATCATGCTGCTCTGCAACTTTTCTATCTGAGCGCATCTAT 1200
 QY 1050 CAAACCAATCTCTACAACTCATTTCAAAGAGTACAGAGCGCGGCTTTAAACTGCT 1109
 Db 1201 CAAACCAATCTCTACAACTCATTTCAAAGAGTACAGAGCGCGGCTTTAAACTGCT 1260
 QY 1110 GCTCGAAGGAAGTCCAGCGCGAGAGGTTTCCACAAGAGAGGACACTGCGGGGGAAGT 1169
 Db 1261 GCTCGAAGGAAGTCCAGCGCGAGAGGTTTCCACAAGAGAGGACACTGCGGGGGAAGT 1320
 QY 1170 TGCAGGGGACACTGGAGAGGACACGCTGGGCTTACACCGAGACAAGCGCTTAAGTCAAGAC 1229
 Db 1321 TGCAGGGGACACTGGAGAGGACACGCTGGGCTTACACCGAGACAAGCGCTTAAGTCAAGAC 1380
 QY 1230 GATGGGATAA 1239
 Db 1381 GATGGGATAA 1390

RESULT 11
 AAF85448
 ID AAF85448 standard; cdNA; 1203 BP.

XX AAF85448;
 AC 23-JUL-2001 (first entry)
 XX Nucleotide sequence of a rabbit motilin receptor polypeptide.
 DE Motilin receptor; gastrointestinal disease; gastric motility disorder;
 KW gastroparesis; irritable bowel syndrome; diarrhoea; ss.
 XX Oryctolagus cuniculus.
 PH Key Location/Qualifiers
 CDS 1..1203
 FT /*tag= a
 FT /note= "motilin receptor"
 XX WO200132710-A1.
 XX 10-MAY-2001.
 XX 25-OCT-2000; 2000WO-US029426.
 XX 29-OCT-1999; 99US-0162264P.
 XX (MERI) MERCK & CO INC.
 XX Tan C, McKee K;
 XX WPI; 2001-343479/36.
 XX P-PSDB; AAB68477.
 XX Novel polypeptides related to dog and rabbit motilin receptor
 PT polypeptide, comprising unique regions from dog and motilin receptor
 PT amino acid sequence, useful for identifying compounds for treating
 PT diarrhea in humans.
 XX Claim 18; Page 18-19; 42pp; English.
 CC The present sequence encodes a rabbit motilin receptor polypeptide. The
 CC specification describes an unique sequence present in exon 1 of the dog
 CC motilin receptor, which is not present in human or Sphaeroides nephelus
 CC 75E7 motilin receptor sequences. The unique nucleic acid sequence is
 CC useful for measuring the ability of a compound to affect motilin receptor
 CC activity. Motilin receptor polynucleotides and polypeptides are used to
 CC identify therapeutic compounds which are useful for treating
 CC gastrointestinal diseases and disorders such as gastric motility
 CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea
 XX SQ Sequence 1203 BP; 154 A; 423 C; 403 G; 223 T; 0 U; 0 Other;
 Query Match 73.9%; Score 915.6; DB 4; Length 1203;
 Best Local Similarity 85.5%; Pred. No. 1.1e-156;
 Matches 1058; Conservative 0; Mismatches 144; Indels 36; Gaps 2;
 QY 1 ATGGGAGCCCTCGAACGGCAGCGCGCCCGCGGGGCGCGGAGCCCGCTGGGCC 60
 Db 1 ATGGGAGCCCTCGAACGGCAGCGCGCCCGCGGGGCGCGGAGCCCGCTGGGCC 60
 QY 61 CGCTGCGCGCTTGGCAGCGCGCGCTGCTGCGCCCTTTCCCTTGGGCGCTGGTGC 120
 Db 61 CGCTGCGCGCTTGGCAGCGCGCGCTGCTGCGCCCTTTCCCTTGGGCGCTGGTGC 120
 QY 121 GTGACCGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 Db 121 GTGACCGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 QY 181 ATGCTGTATCGGGCGCTACCGGGACATGCGGACACCACTTGTACTTGGGAGCATG 240
 Db 181 CTGCTGTATCGGGCGCTACCGGGACATGCGGACACCACTTGTACTTGGGAGCATG 240
 QY 241 GCGGTGTCCGACCTACTCATCTGCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 300

241	Db	GC	GTGTCGACCTGCTCATCTCTGCTCGGGCTGCCCTTCGACCTGTATACCGCTGTGTGGCGC	300
301	Qy	TC	CGGGCCCTGGGTGTTTCGGGCGCGCTGCTCTGCGCGCCTGTGCTCTACGTGGGCGAGGGC	360
301	Db	TC	GAGGCCCTGGGTGTTTCGGACAGCTGCTCTGCGCGCTGTGCTGTACGTGGGCGAGGGC	360
361	Qy	TG	CACCTACGCCAGCGTGTGCACATACACCGCGCTCAGCGTTCAGAGCGCTACCTGGCCATC	420
361	Db	TG	CACCTACGCCCTCGCTGTGTCACATACACCGCGCTCAGCGTTCAGAGCGCTACCTGGCCATC	420
421	Qy	TG	CGCGCGCTTCGCGCGCGCGTCTTCGTTCACCCGCGCGCGCTGCTGCGCGCTCATCGCT	480
421	Db	TG	CGCGCGCTTCGTGTCGCGCGCTTCGTTCACCCGCGCGCGCTGCTGCGCGCTCATCGCT	480
481	Qy	GT	GCTCTGGGCGTGGCGCTGCTCTCTGCGGTCCTTCTTGTTCCTGGTGGGCGTTCGAG	540
481	Db	GC	GCTCTGGGCGTGGCGCTGCTTTCGCGCGGCGCTTCTTCTTCTGTGTGGGCGTTCGAG	540
541	Qy	CAG	ACCCCGGCATCTCGTAGTCCCGGGCTCAATGGCACCGCGCGGATCGCCTCTCTG	600
541	Db	CAG	ACCCCGCGGTCTTCGCGGCGCGCGACCGCAACGCTACTGTGCGCGCTGGAACCCCTCG	600
601	Qy	CT	CTCGCCTCTGTCGCGCGCTCTCTGCTCTCGCGGCGGCACCGCGCTGCCCGCGCTCG	660
601	Db	TC	CGCGCC-----CGGCGTCTCCCGCGCTCG	627
661	Qy	GG	CGCGAGACCGCGAGCGCGCGCTGTTCAGCGCGAATGCGCGCGCAGCCCGCGC	720
628	Db	GG	CGCG---GAGCGAGGCGCGGCTCTGTTCAGCGCGAGTGCAGCGCGCGCGCGCGC	684
721	Qy	CAG	CTGGCGCGCTGCGGTGTCATGCTGTGGTTCACACCGCTACTTCTTCTGGCCCTTT	780
685	Db	CAG	CTGGGCTTGTCTGCGCGTCTGCTGTGGTTCACACCGCTACTTCTTCTGGCCCTTC	744
781	Qy	CT	GTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCCGCGGCGCG	840
745	Db	CT	TGCTCAGCATCTCTACGGGCTCATCGCGCGGAGCTGTGGCGGGTGTGGGCGCGC	804
841	Qy	CT	CGAGGCCCGCGCGCTCGGGCGGGAGAGGCCACCGCGCAGACCGTCCGCGTCTTG	900
805	Db	CT	CGAGGCCCGCGCGCACCGGTCGGGAGAGGGGCCACCGCGCAGACCGTCCGCGTCTTG	864
901	Qy	CT	GGTGGTGTCTGGCATTTTAAATTTGCTGGTTGCGCTTCCACGTTGGCAGNATCATTT	960
865	Db	CT	GGTGGTGTCTGGCCTTTATAGTGTGTGCTGCTTTCACGTTGGCAGGATCATTT	924
961	Qy	TA	CATAAACACGGAAGATTCCGGATGATGTACTTCTCTCAGTACTTTAAACATCGTCGT	1020
925	Db	TA	CATAAACACCCAGACTTCGGGATGATGTACTTCTCCAGTACTTTAACTGTGCG	984
1021	Qy	CT	GAACTTTTCTATCTGAGCGCATCTATCAACCCAAATCTCTACAACTCATTTCAAAG	1080
985	Db	CT	GAGCTTTTCTACCTGAGTGGCTCCATCAACCCAAATCTCTACAACTCATCTCCNAG	1044
1081	Qy	AA	GTACAGAGGGCGGCTTTAACTGCTGCTCGCAGGAAGTCCAGCGCGAGAGGCTTC	1140
1045	Db	AA	GTACAGAGCGGCTGCCCGAGACTGCTGCGGAAAGCCGAGCGGGCGCCAGTGGTGTG	1104
1141	Qy	CA	CAGAAGCAGGGACACTGCGGGGGAAGTTGTCAGGGGACACTGGAGGAGACACGTGGCG	1200
1105	Db	TG	CGGAAGCAGGGCCCTGAGACGACGTTGTCAGGGGACACTGGCGAGACACAGCTGGC	1164
1201	Qy	TAC	CACGAGACAAGCGCTAACGTGAAGACGATGGGATA	1238
1165	Db	TG	CACCGAGACCAAGCGCTTAACAACGAGCGCTGCATA	1202

RESULT 12
AAF83684
ID AAF83684
XX
AC
XX

DT	23-JUL-2001	(first entry)
XX	Short form of motilin receptor, GPR-38B isoform encoding DNA.	
XX	zsig33; signal transduction; hormone; enzyme; neural development;	
XX	gastric contractility; nutrient uptake; digestive; pancreatic; human;	
KW	insulin-like growth factor-I; growth hormone; bone; gastrointestinal;	
KW	glucose; osteopathic; anorectic; vulnerable; immunomodulator; GHS-R; da;	
XX	G-protein coupled receptor; motilin receptor; GPR38; GPR38B; isoform.	
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
FH	CDS	1..1161
FT	FT	/*tag= a
FT	FT	/product= "GPR-38B"
XX	W0200138355-A2.	
XX	31-MAY-2001.	
PD	22-NOV-2000;	2000WO-US032074.
PF	22-NOV-1999;	99US-0166765P.
XX	(ZYMO) ZYMOGENETICS INC.	
XX	Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;	
XX	WPI; 2001-355879/37.	
DR	P-PSDB; AAB62653.	
XX	Forming reversible peptide receptor complex for purifying cell and	
PT	peptides, stimulating signal transduction and modulating hormone	
PT	secretion, involves contacting a receptor with zsig33 polypeptide.	
XX	Disclosure; Page 106-109; 111pp; English.	
XX	The invention relates to a method of forming a reversible peptide-	
CC	receptor complex that involves providing an immobilized receptor, and	
CC	contacting the receptor with a zsig33 peptide (comprising residues 24-37	
CC	of AAB62649), where the receptor binds to the zsig33 peptide. The method	
CC	is useful for purifying cells, purifying a peptide, stimulating signal	
CC	transduction in a cell expressing a receptor. It is also useful for	
CC	modulating secretion of hormones, neural development and/or utilization,	
CC	gastric contractility, nutrient uptake, secretion of digestive and	
CC	pancreatic enzymes and hormones, secretion of insulin-like growth factor	
CC	-I, secretion of non-zsig33 proteins. It is useful for modulating growth	
CC	hormone secretion in a mammal having a disease associated with abnormal	
CC	levels of growth hormone, such as osteoporosis, bone repair, bone	
CC	remodeling, low osteoblast levels, cartilage repair and remodeling,	
CC	skeletal dysplasia, immune suppression, obesity, growth retardation,	
CC	protein catabolic responses after surgery, cachexia, protein loss,	
CC	dwarfism, wound healing and ovulation induction, treating a mammal having	
CC	a metabolic disorder requiring neurological feedback, such as satiety	
CC	regulation, glucose absorption and metabolism and neuropathy-associated	
CC	gastrointestinal disorders, and stimulating glucose-induced insulin	
CC	release in a mammal. The present sequence represents the DNA encoding the	
CC	short form of motilin receptor, GPR-38B (one of the two isoforms of GPR38	
CC	which result from alternative splicing). GPR38 has homology to the human	
CC	G-protein coupled receptor, GHS-R	
XX	Sequence 1161 BP; 126 A; 436 C; 372 G; 227 T; 0 U; 0 Other;	
XX	Query Match 72.7%; Score 901; DB 4; Length 1161;	
XX	Best Local Similarity 100.0%; Pred No. 4.9e-154;	

[illegible]


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QY 241 GCGGTGCGGACCTACTCTCTGCTCGGCTCGGCTTCCGACTGTACCGCTCTGGCGC 300
DB 1269 GCGGTGCGGACCTACTCTCTGCTCGGCTCGGCTTCCGACTGTACCGCTCTGGCGC 1328
QY 301 TCGCGGCTTGGGTGTTGGGCGCGCTGCTCTGCGGCTCTTCCCTCTACGTGGCGAGGC 360
DB 1329 TCGCGGCTTGGGTGTTGGGCGCGCTGCTCTGCGGCTCTTCCCTCTACGTGGCGAGGC 1388
QY 361 TGACCTAGCCACGCTGTCACATGACCGGCTCAGCGTGCAGGGCTACCTGGCCATC 420
DB 1389 TGACCTAGCCACGCTGTCACATGACCGGCTCAGCGTGCAGGGCTACCTGGCCATC 1448
QY 421 TCGCGGCTTGGGTGTTGGGCGCGCTGCTCTGCGGCTCTTCCCTCTACGTGGCGAG 480
DB 1449 TCGCGGCTTGGGTGTTGGGCGCGCTGCTCTGCGGCTCTTCCCTCTACGTGGCGAG 1508
QY 481 GTGCTTGGGCGCTGCGGCTGCTCTGCGGCTCTTCCCTCTACGTGGCGAG 540
DB 1509 GTGCTTGGGCGCTGCGGCTGCTCTGCGGCTCTTCCCTCTACGTGGCGAG 1568
QY 541 CAGGACCCGCGATCTCCGTAGTCCGCGGCTCAATGGCACCGCGGATCGCTCCGCG 600
DB 1569 CAGGACCCGCGATCTCCGTAGTCCGCGGCTCAATGGCACCGCGGATCGCTCCGCG 1628
QY 601 CTTCTCGCTGCTGCGGCTCTCTGCTCTGCGGCTCAGCGGCTCAGCGGCTCGG 660
DB 1629 CTTCTCGCTGCTGCGGCTCTCTGCTCTGCGGCTCAGCGGCTCAGCGGCTCGG 1688
QY 661 GGGCGGACCGCGAGCGCGGCTGTTAGCGCGGATGCGCGGAGCGCGCG 720
DB 1689 GGGCGGACCGCGAGCGCGGCTGTTAGCGCGGATGCGCGGAGCGCGCG 1748
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DB 1749 CAGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1808
QY 781 CTGTGCTCAGATCTCTACGGCTCTACGGCTCTACGGCTCTACGGCTCTACGGCT 840
DB 1809 CTGTGCTCAGATCTCTACGGCTCTACGGCTCTACGGCTCTACGGCTCTACGGCT 1868
QY 841 CTGCGAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 1869 CTGCGAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1928
QY 901 C 901
DB 1929 C 1929

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RESULT 15

ADG70447_0
 WP Sequence split into 5 fragments LOCUS ADG70447 Accession Adg70447

WP	Fragment Name	Begin	End
WP	ADG70447_0	1	110000
WP	ADG70447_1	100001	200000
WP	ADG70447_2	200001	310000
WP	ADG70447_3	300001	410000
WP	ADG70447_4	400001	410846

ID ADG70447 standard; DNA; 410846 BP.

XX AC ADG70447;

XX ADG70447;

DT 11-MAR-2004 (first entry)

XX Human ANGE-CLLD8-CLLD7 hybrid gene.

XX ANGE, CLLD8; CLLD7; ANGE-CLLD8; ANGE-CLLD7; CLLD7-CLLD8;

KW ANGE-CLLD8-CLLD7; anti-allergic; antiasthmatic; dermatological;

KW antipyretic; antiinflammatory; gene therapy; IGE-mediated disease;

KW ANGE 1; single nucleotide polymorphism; ds.

XX Chimeric.

OS Homo sapiens.

XX Key Location/Qualifiers
 variation replace(186655,G)
 FT /*tag= a
 /*standard_name= "Single nucleotide polymorphism"
 FT replace(338770,G)
 /*tag= b
 /*standard_name= "Single nucleotide polymorphism"
 FT replace(360186,G)
 /*tag= c
 /*standard_name= "Single nucleotide polymorphism"

XX WO2003000727-A2.

XX 03-JAN-2003.

XX 21-JUN-2002; 2002WO-GB002859.

XX 21-JUN-2001; 2001GB-00015211.

XX 21-JUN-2001; 2001GB-00015212.

XX 21-JUN-2001; 2001GB-00015213.

XX (ISIS-) ISIS INNOVATIONS LTD.

XX Zhang Y, Moffatt M, Cookson W, Tinsley J;

XX WPI, 2003-201405/19.

XX New nucleic acid sequence comprising an ANGE, CLLD8 or CLLD7 mRNA, or their hybrid, useful for screening agents for treating IGE-mediated diseases, e.g. asthma, atopy, hay fever, eczema, atopic dermatitis, or allergic rhinitis.

XX Claim 12; Fig 5; 429pp; English.

XX The invention relates to a novel isolated or recombinant nucleic acid sequence comprising an ANGE, CLLD8 or CLLD7 mRNA, or ANGE-CLLD8, ANGE-CLLD7, CLLD7-CLLD8, or ANGE-CLLD8-CLLD7 hybrid mRNA sequence, its complement, homologue or fragment. The novel nucleic acid sequences have the following activities: anti-allergic, antiasthmatic, dermatological, antipyretic, and antiinflammatory. The nucleic acids of the invention may be used in gene therapy to treat disorders. The nucleic acid sequences are useful for screening agents that inhibit or enhance activity of an ANGE, CLLD8 or CLLD7 gene. The agent or antibody is useful for treating IGE-mediated diseases, such as asthma, atopy, hay fever, eczema, atopic dermatitis, allergic rhinitis or non-atopic asthma. The antibody is useful in an assay detecting or measuring the polypeptide in the sample. The host cell is useful for producing, regulating and analyzing the polypeptide. The splice variant of ANGE, CLLD8, or CLLD7 is useful for diagnosing an IGE-mediated disease, atopy, a form of atopic disease or non-atopic asthma, or predicting the severity, or predisposition to a disease. This polynucleotide sequence represents the human ANGE-CLLD8-CLLD7 hybrid gene of the invention.

XX Sequence 410846 BP; 125178 A; 83171 C; 81704 G; 120793 T; 0 U; 0 Other;

XX Query Match 72.7%; Score 901; DB 10; Length 110000;

XX Best Local Similarity 100.0%; Pred. No. 6.3e-154;

XX Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 38016 ATGGGACGCCCTTGAAACGGACGACGCGCCCGGAGGGGCGCGGAGCGCGCC 38075

QY 61 GCGGTGCGGCTTCCGAGCGCGCTGCTCGCCCTTTCCCTGGGGGCGCTGGTCCG 120

DB 38076 GCGGTGCGGCTTCCGAGCGCGCTGCTCGCCCTTTCCCTGGGGGCGCTGGTCCG 38135

QY 121 GTGACCCGCTGTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

DB 38136 GTGACCCGCTGTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 38195

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:51:55 ; Search time 203.635 Seconds
(without alignments)
9955.765 Million cell updates/sec

Title: US-09-719-485-2

Perfect score: 1239

Sequence: 1 atgggcagccctggaacgg.....acgtgaagacatgggataa 1239

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	22.8	283	3	US-08-993-088A-4
2	283	22.8	283	3	US-08-993-424B-4
3	283	22.8	283	4	US-09-603-680-4
4	255.8	20.6	1050	4	US-09-762-661A-1
5	234.8	19.0	1063	3	US-09-077-675A-1
6	234.8	19.0	1063	4	US-09-077-674-1
7	231.6	18.7	1095	4	US-09-743-475-2
8	231.6	18.7	4009	4	US-09-743-475-1
9	230	18.6	1029	3	US-09-077-675A-4
10	230	18.6	1029	4	US-09-077-674-4
11	229.8	18.5	1092	3	US-09-077-675A-15
12	229.8	18.5	1092	4	US-09-077-674-15
13	229	18.5	250	4	US-09-016-434-359
14	228.8	18.5	1122	3	US-09-077-675A-9
15	228.8	18.5	1122	4	US-09-077-674-9
16	228.4	18.4	3129	3	US-09-077-675A-14
17	228.4	18.4	3129	4	US-09-077-674-14
18	227.8	18.4	1088	3	US-09-077-675A-6
19	227.8	18.4	1088	4	US-09-077-674-6
20	227.8	18.4	1101	4	US-09-016-434-1148
21	227.8	18.4	1101	4	US-09-170-496D-87
22	227.8	18.4	1101	4	US-09-170-496D-209
23	227.8	18.4	1101	4	US-09-364-425B-44
24	153	12.3	836	3	US-09-077-675A-11
25	153	12.3	836	4	US-09-077-674-11
26	134.8	10.9	729	4	US-09-684-725-1
27	134.8	10.9	1239	4	US-09-949-016-4230

28 134.8 10.9 1248 3 US-09-545-944-1 Sequence 1, Appli
29 134.8 10.9 1360 4 US-09-341-016A-2 Sequence 2, Appli
30 134.8 10.9 16914 4 US-09-949-016-15972 Sequence 15972, A
31 132 10.7 1575 3 US-08-858-876A-1 Sequence 1, Appli
32 132 10.7 1575 3 US-09-472-880-1 Sequence 1, Appli
33 127.2 10.3 1233 4 US-08-826-509-536 Sequence 536, App
34 125.4 10.1 1342 3 US-08-832-399-1 Sequence 1, Appli
35 125.4 10.1 1342 3 US-09-372-498-1 Sequence 1, Appli
36 123 9.9 1257 4 US-09-826-509-534 Sequence 534, App
37 123 9.9 4080 4 US-09-016-434-1346 Sequence 1346, Ap
38 122.8 9.9 1529 3 US-08-858-876A-3 Sequence 3, Appli
39 122.8 9.9 1529 3 US-09-472-880-3 Sequence 3, Appli
40 122 9.8 1095 4 US-08-826-509-576 Sequence 576, App
41 122 9.8 1285 4 US-09-016-434-1366 Sequence 1366, Ap
42 120.4 9.7 1233 3 US-09-200-090-1 Sequence 1, Appli
43 120 9.7 1535 3 US-09-668-680-12 Sequence 12, Appl
44 119 9.6 1212 4 US-09-170-496D-113 Sequence 113, App
45 119 9.6 1212 4 US-09-170-496D-223 Sequence 223, App

ALIGNMENTS

RESULT 1

US-08-993-088A-4
; Sequence 4, Application US/08993088A
; Patent No. 6287855
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Sullivan, Kathleen
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,088A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...283
; OTHER INFORMATION: cdna probe
US-08-993-088A-4

Query Match 22.8%; Score 283; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 4.4e-50;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 TCGGACACCAACCACTTGTACCTGGGAGAGATGGCGCTGCCAGCTACTCATCTCTGC 265
Db 1 TCGGACACCAACCACTTGTACCTGGGAGAGATGGCGCTGCCAGCTACTCATCTCTGC 60

QY 266 TCGGGCTGCGGTTTCGACCTGTACCGCTCTGGGCTTGGGCGCTGGGTTTCGGGCGGC 325
Db 61 TCGGGCTGCGGTTTCGACCTGTACCGCTCTGGGCTTGGGCGCTGGGTTTCGGGCGGC 120

QY 326 TGTCTGCGGCTGTCCCTCTACCTGAGGAGGCTGCACCTACGCGCTGCTGCACA 385
Db 121 TGTCTGCGGCTGTCCCTCTACCTGAGGAGGCTGCACCTACGCGCTGCTGCACA 180

QY 386 TGACCGCGCTCAGCGTCGAGCGTACCTGGCCATCTGCGCGCGCTTCCGCGCGCGGCT 445
Db 181 TGACCGCGCTCAGCGTCGAGCGTACCTGGCCATCTGCGCGCGCTTCCGCGCGCGGCT 240

QY 446 TGTACCCCGCGCGCTTCCGCGCGCTCATCGCTGCTCTG 488
Db 241 TGTACCCCGCGCGCTTCCGCGCGCTCATCGCTGCTCTG 283

RESULT 2

US-08-993-424B-4
; Sequence 4, Application US/08993424B
; Patent No. 6337206
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Kolakowski, Lee F., Jr.
; TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALR2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,424B
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846NP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...283
; OTHER INFORMATION: cDNA probe

US-08-993-424B-4

Query Match 22.8%; Score 283; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 4.4e-50;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 TCGGACACCAACCACTTGTACCTGGGAGAGATGGCGCTGCCAGCTACTCATCTCTGC 265
Db 1 TCGGACACCAACCACTTGTACCTGGGAGAGATGGCGCTGCCAGCTACTCATCTCTGC 60

QY 266 TCGGGCTGCGGTTTCGACCTGTACCGCTCTGGGCTTGGGCGCTGGGTTTCGGGCGGC 325
Db 61 TCGGGCTGCGGTTTCGACCTGTACCGCTCTGGGCTTGGGCGCTGGGTTTCGGGCGGC 120

QY 326 TGTCTGCGGCTGTCCCTCTACCTGAGGAGGCTGCACCTACGCGCTGCTGCACA 385
Db 121 TGTCTGCGGCTGTCCCTCTACCTGAGGAGGCTGCACCTACGCGCTGCTGCACA 180

QY 386 TGACCGCGCTCAGCGTCGAGCGTACCTGGCCATCTGCGCGCGCTTCCGCGCGCGGCT 445
Db 181 TGACCGCGCTCAGCGTCGAGCGTACCTGGCCATCTGCGCGCGCTTCCGCGCGCGGCT 240

QY 446 TGTACCCCGCGCGCTTCCGCGCGCTCATCGCTGCTCTG 488
Db 241 TGTACCCCGCGCGCTTCCGCGCGCTCATCGCTGCTCTG 283

RESULT 3

US-09-603-680-4
; Sequence 4, Application US/09603680
; Patent No. 6544753
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Sullivan, Kathleen
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/603,680
; FILING DATE: 26-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; APPLICATION NUMBER: 08/993,088
; FILING DATE: 18-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846 CA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other

Qy	212	CCACCAACAACTTGTATCTGGGAGCATGCCCGTGTCCGACCTACTCATCTCTGTCGGGC	271
Db	176	CCACCAACAACTGTACTCTGACGCTGGCCCTGCTCCGACCTGCTCATCTTCTCTGTGCA	235
Qy	272	TGCGGTTCGACCTGTACCGCCTCTGGGGCTCGGGGCCCTGGGTGTTTCGGGGCCGTGCTCT	331
Db	236	TGCGCTTCGACCTGGTGGCGCTGTGGCAGTACCGGCCCTGGACCTTCGGGACCTGCTCT	299
Qy	332	GCCGCTGTCCCTCTACGTGGGAGGGGTGCACCTACGCCACGCTGCTGCACATGACCG	391
Db	296	GCAACTCTTCCAGTTCTGAGCGAGGGCTGACCTACGCCACGGTGTCAACATCAGG	355
Qy	392	CGCTCAGCGTCGAGCGCTACTCGGCCATCTGCGCCCGCTCCGGCCCGCTCTTGTCGA	451
Db	356	CGCTGAGCGTCGAGCGCTACTTCGCCATCTGCTTCCGCTCGGGCCCAAGTGTCTGTGA	415
Qy	452	CCGGCGCCGCTCCGCGCGCTCATCGCTGTGCTCTGGGCGTGGGCGCTGCTCTCTGCGG	511
Db	416	CCAAGGCGCGCTGAAGTGGCCCTGTGGCCATCTGGGCGTGGCCCTTCTGCAGCGCGG	475
Qy	512	GTCCCTCTTGTTCTTGTTGGGCGTCGAGCAGGACCCGGGCATCTCGTAGTCCCGGGCC	571
Db	476	GGGCCATCTTCTGCTGCTGGTGGGCTGGAGCACGAGAACGGCACC-----	519
Qy	572	TCAATGGCACCGCGCGGATCGCTCTCTCGCCTCTCGCCCTCTCTGCGCGCTCTCTGCTGCTCT	631
Db	520	-----GACCC	524
Qy	632	CGCGGGCGCCACCGCGCTCCCGCGTCCGGGGCCCGAGACCGCGGAGGGCCGCGCGGTGT	691

692	TCAGCCGCGAATGCGCGCGAGCGCCGCGAGCTGGCGCGCTGCGTGCATGCTGTGGG	751
560	-----CGTGGCTCGGGGCTGCTCACGCCCATGTTGTGGG	595
752	TCACCACCGCTACTTCTTCCTGCCCTTCTGTGCGCTCAGCATCCTCTACGGGCTCATCG	811
596	TGTCCAGCGTCTTCTTCTTCCTGCCGCTCTTGTGCTCAGCGTGCTCTACGGCTCATCG	655
812	GGCGGAGCTGTGGAGCAGCGCGGCGCGCTGGAGCGCCGCGCGCTCGGGCGGGAGA	871
656	GCAGGAAGCTGTGGCGCGGGGCGCGGCACACNGCGGGGGCGCTCGCTCCGCGAGC	715
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716	AGAGCCACCCGCGCAGACGGTGAAGATGCTCGCTGTGCTGTGTTTTCATCTTCTGCT	775
932	GGTTGCCCTTCCACGTGTGGCAGA-----ATCATTTACATAAACACGGGAAGATTGCG	982
776	GGCTGCCCTTCCACGTGGGGCGATATTTATTTCCAAAGTCTTCGAGCCCGGCTCCTTGG	835
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836	AGATTGCTCAGATCAGCCAACTATGCAACCTGGTATCCTTTGTCTCTTCTTACCTCAGTG	895
1043	CATCTATCAACCCAAATCCTCTACAACCTCATTTTCAAAGAAGTACAGAGCGCGGCCCTTTA	1102
896	CTGCCATCAATCCATTCTGTACAACATCATGTCCAAAGAAGTACCGGGTGGCGGTGTTC	955

QY	1103	AAUGGCG	1110
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Qy	152	TCCGGGTGAGCGGCACGTGGTGACCGGTGCTGCTGATCGGGCGCTACCGGACATCGGA	211						
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Qy	212	CCACCACCAACTTGTACCTGGGCACATGGCGGTGTCGGACCTACTCATCTGCTCGGGC	271						
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Qy	272	TGCGGTTCGACCTGTACCGCCTCTGGCGCTCGCGCCCTGGGTTCGGCGCGCTGCTCT	331						
Db	284	TGCGGTGACACTCGTCGCCCTCTGGCAGTATCGGCCCTGGAATTCGGCGACCTGCTCT	343						
Qy	332	GCGCCCTGTCCCTCTACGTGGGCGAGGGCTGCACCTACGCCACGCTGCTGCACATACCG	391						
Db	344	GCAAACTCTCCAGTTGTTCAGGAGAGCTGCACCTACGCCACGGTCTCTACCATCACCG	403						
Qy	392	CGCTCAGCGTTCGAGCGCTACTTGGGCCATCTGCGCGCGCTCCGCGCCCGGTCTTGGTCA	451						

Query Match	18.7%	Score	231.6	DB	4	Length	4009
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Gaps	0						
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Qy	152	TCGGGGTGAGCGGCAACGTGGTCAACCGTGATCGGGCGCTACCGGGACATCGCGA	211				
Db	665	TGGCATCTCGGGCAACCTGCTACCATGCTGGTGGTGCCCGCTTCGGGAGCTGGCA	724				
Qy	212	CCACCAACAACTGTGTACCTGGGAGAGATGCCGTGTCCGACCTACTATCTCTCTCGGGC	271				
Db	725	CCACCAACAACTCTACTATCCAGATGAGCCCTTCCGATCTGCTCATCTTCTCTGCA	784				
Qy	272	TGCGTTTCGACCTGTACCGCTCTGCGCTCGCGGCCCTGGGTGTTCGGGCGCTGCTCT	331				
Db	785	TGCGCTGGACCTCGTCCGCTCTGGAGTATCGGCCCTGGAACTTCGGGACCTGCTCT	844				
Qy	332	CGCGCTGTCCCTCTACGTGGGCGAGGCTGCACTACGCACGCTGCTGCATGACCG	391				
Db	845	GCAAACTCTTCCAGTTTGTTCAGCGAGAGCTGCACTACGCCACGGTCTCACCATCACCG	904				
Qy	392	CGCTCAGCGTGCAGCGTACTGGGCATCTGCCCGCGCTCCGGCGCGCGGTCTTGGTCA	451				
Db	905	CGCTGAGCGTGCAGCGCTACTTCGCCATCTGCTTCCGCTCGCGGGCAAGTGGTGGTCA	964				
Qy	452	CCGGCGCCGCGTCCGGCGCTCATCGCTGTGCTCTGGGCGGTGGCGCTGCTCTGCGCG	511				
Db	965	CCAAGGCGGTGGAAGCTGGTCACTCTTGTCACTTGGGCGGTGGCTTCTGCAGCGCGG	1024				
Qy	512	GTCCCTTCTTGTTCCTGGTGGCGTCCAGACGAGCCCCGGCA	553				


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NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P. O. Box 2000, 126 B. Lincoln Ave
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
FILING DATE: 3-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19590P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-077-675A-9

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Query Match	18.5%	Score 228.8	DB 3	Length 1122
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Db	360	GCCTTTCCCGCGCGCTGTCTGGCGGGCGGTACAGCCACCTTCGCTGGCACTCTTCGTGGT	419	
Qy	153	CGGGGTGAGCGGCAACGTGGTGTGACCGGTGATGCTGATCGGGCGCTACCGGGACATCGGCAC	212	
Db	420	GGGTATCGCTGGCAACCTGCTCACCATGCTGGTGTGTCGCGCTTCGCGAGCTCGGCAC	479	
Qy	213	CACACCAACTGTACTCTGGCGAGCATGGCGGTCTCGACCTACTCATCTGCTCGGGCT	272	
Db	480	CACACCAACTCTACTCTGTCCAGCATGGCGCTTCTCCGATCTGTCTCATCTTCTCTGCAT	539	
Qy	273	GCGGTTTCGACCTGTACCGCTCTGGCGCTCGCGGCCCTGGGTGTTCGGGCGCGCTCTCTG	332	
Db	540	GCCCTTGGACCTCGTTGCCTCTGGCAGTACCGGCCCTTGGAACTTCGGCGGACCTCTCTG	599	
Qy	333	CGSCCTGTCCCTCTAGTGGCGGAGGCTGCACCTAGCCACGCTGTGCAATGACCGC	392	
Db	600	CAAACTCTTCCAATTCGTAGTGAGAGCTGCACCTAGCCACGGTGTCTCACCATCACAGC	659	
Qy	393	GCTCAGGTCGAGCGCTACTGCGGCATCTCCGCGCGCTTCGCGCCCGCGCTTCGTGTCAC	452	
Db	660	GCTGAGCGTCGAGCGCTACTTCGCGCATCTGCTTCCCACTCCGGGCGCAAGGTGGTGGTTCAC	719	
Qy	453	CCGGCGCGCGCTCCGCGCGCTCATCTGCTGTGCTCTGGGCGCGTGGCGCTCTCTTCGCGGG	512	
Db	720	CAAGGGCGGGTGAAGCTGTGTCATCTTCGTTCATCTGGGCGCTGGCTTCTCGAGCGCGG	779	
Qy	513	TCGCTTCTTGTTCCTGGTGGGCTCGAGCAGGACCCCGGCACT-CCGTAGTCCCGGGCC	571	
Db	780	GCCCATCTTTCGTGTAGTTCGGGGTGGAGCACGAGAACGGCACCGACCTCTGGGACACCAA	839	

[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 06:41:42 ; Search time 723.385 Seconds
(without alignments)
10379.464 Million cell updates/sec

Title: US-09-719-485-2
Perfect score: 1239
Sequence: 1 atggcgagccctggaacgg.....acgtgaagacatgggataa 1239

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239	100.0	1239	15	US-10-225-567A-472
2	1239	100.0	1239	15	US-10-290-078-13
3	1239	100.0	1239	15	US-10-290-078-14
4	1239	100.0	1239	16	US-10-206-677-1
5	1239	100.0	1239	18	US-10-679-813-9
6	901	72.7	1161	18	US-10-679-813-11
7	896.2	72.3	2040	10	US-09-876-252-129
8	896.2	72.3	2040	17	US-10-417-820A-129
9	896.2	72.3	2040	18	US-10-723-955-129
10	891.4	71.9	2040	17	US-10-417-820A-151
c 11	501.2	40.5	1179	18	US-10-363-345A-33737

c 12	501.2	40.5	1179	18	US-10-363-345A-33738	Sequence 33738, A
c 13	501.2	40.5	1179	19	US-10-363-483A-33737	Sequence 33737, A
c 14	501.2	40.5	1179	19	US-10-363-483A-33738	Sequence 33737, A
c 15	437.2	35.3	1179	18	US-10-363-345A-33739	Sequence 33739, A
c 16	437.2	35.3	1179	18	US-10-363-345A-33740	Sequence 33740, A
c 17	437.2	35.3	1179	19	US-10-363-483A-33739	Sequence 33739, A
c 18	437.2	35.3	1179	19	US-10-363-483A-33740	Sequence 33740, A
c 19	230	19.0	1063	16	US-10-303-204A-4	Sequence 1, Appli
c 20	230	18.6	1029	16	US-10-303-204A-1	Sequence 4, Appli
c 21	229.8	18.5	1092	16	US-10-303-204A-15	Sequence 15, Appli
c 22	229	18.5	250	17	US-10-305-720-359	Sequence 359, App
c 23	228.8	18.5	870	15	US-10-225-567A-139	Sequence 139, App
c 24	228.8	18.5	1122	16	US-10-303-204A-9	Sequence 9, Appli
c 25	228.4	18.4	3129	16	US-10-303-204A-14	Sequence 14, Appli
c 26	227.8	18.4	1088	16	US-10-303-204A-6	Sequence 6, Appli
c 27	227.8	18.4	1101	15	US-10-251-385-87	Sequence 87, Appli
c 28	227.8	18.4	1101	15	US-10-251-385-209	Sequence 209, App
c 29	227.8	18.4	1101	16	US-10-276-392-22	Sequence 22, Appli
c 30	227.8	18.4	1101	17	US-10-305-720-1148	Sequence 1148, Ap
c 31	227.8	18.4	1101	18	US-10-679-813-4	Sequence 4, Appli
c 32	187.4	15.1	1098	18	US-10-679-813-6	Sequence 6, Appli
c 33	153	12.3	836	16	US-10-303-204A-11	Sequence 11, Appli
c 34	134.8	10.9	729	18	US-10-915-157-1	Sequence 1, Appli
c 35	134.8	10.9	801	10	US-09-782-374C-17	Sequence 17, Appli
c 36	134.8	10.9	801	19	US-10-467-492A-17	Sequence 556, App
c 37	134.8	10.9	1239	15	US-10-225-567A-556	Sequence 2, Appli
c 38	134.8	10.9	1245	18	US-10-203-015A-2	Sequence 18, Appli
c 39	134.8	10.9	1245	18	US-10-203-015A-18	Sequence 11, Appli
c 40	134.8	10.9	1248	10	US-09-875-076-11	Sequence 11, Appli
c 41	134.8	10.9	1248	10	US-09-876-252-11	Sequence 11, Appli
c 42	134.8	10.9	1248	15	US-10-272-983-11	Sequence 11, Appli
c 43	134.8	10.9	1248	16	US-10-393-807-11	Sequence 11, Appli
c 44	134.8	10.9	1248	17	US-10-417-820A-11	Sequence 11, Appli
c 45	134.8	10.9	1248	18	US-10-723-955-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1

US-10-225-567A-472
; Sequence 472, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 472
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-472

Query Match	100.0%	Score 1239;	DB 15;	Length 1239;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1239;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGCGAGCCCTTGGACGAGCGCGCCCGAGGGGGCGCGGAGCCCGTGGGCC 60		
Db	1	ATGGCGAGCCCTTGGACGAGCGCGCCCGAGGGGGCGCGGAGCCCGTGGGCC 60		
Qy	61	CGCTGCGCGCTTGGACGAGCGCGCTGTGCGCCCTTCCCTGGGGGGCGTGTGCGG 120		
Db	61	CGCTGCGCGCTTGGACGAGCGCGCTGTGCGCCCTTCCCTGGGGGGCGTGTGCGG 120		


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Db 661 GGGCCGAGACGGCGGAGCGCGCGCTGTTCAGCCGGAATGCCGCGCGAGCCCGCG 720
Qy 721 CAGCTGGGCGCGCTCGCTGTATGCTGTGGGTACACACCGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGGCGCGCTCGCTGTATGCTGTGGGTACACACCGCTACTTCTTCTGCGCTTT 780
Qy 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGCGCG 840
Db 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGCGCG 840
Qy 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCGTCGGTCTG 900
Db 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCGTCGGTCTG 900
Qy 901 CTGTGTGTGTCTGCGCATTTATAATTTGCTGTTGCCCTTCCAGTTGGCAGATCAT 960
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Qy 961 TACATAAACAAGGAGATTCGCGGATGATCTCTCAGTACTTTTAAACATCGTCT 1020
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Db 1141 CACAGAAGCAGGACACTCGCGGGAAGTTGCGGGGACACTGGAGGAGACACGTTGGC 1200
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RESULT 3

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US-10-290-078-14
; Sequence 14, Application US/10290078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE OF INVENTION: 14395, 14618, 17692 or 58874
; FILE REFERENCE: MPI2001-288P1(M)
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-290-078-14
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Query Match 100.0%; Score 1239; DB 15; Length 1239;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 ATGTGATCGGGCGCTACCGGGAATGCGGGAACACCACTTGTACCTGGGCGAGCATG 240
Db 181 ATGTGATCGGGCGCTACCGGGAATGCGGGAACACCACTTGTACCTGGGCGAGCATG 240
Qy 241 GCCGTGTCGACCTACTCATCTGCTGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCT 300
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Db 301 TCGGCGCGCTGGGTGTTTCGGGCGCGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTG 360
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Qy 421 TCGCGCGCGCTGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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Db 721 CAGTGGGCGCGCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
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Db 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGCGCGCG 840
Qy 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCGTCGGTCTG 900
Db 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCACCGGACAGCGTCGGTCTG 900
Qy 901 CTGTGTGTGTCTGCGCATTTATAATTTGCTGTTGCCCTTCCAGTTGGCAGATCAT 960
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Qy 961 TACATAAACAAGGAGATTCGCGGATGATCTCTCAGTACTTTTAAACATCGTCT 1020
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Qy 1021 CTGCAACTTTTCTATCTAGCGCATCTATCAACCCCAATCCTCTACAACCTCAT 1080
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Qy 1081 AAGTACAGAGCGCGCGCTTTAAACTGCTGCTCGCAAGGAAGTCCAGGCGGAGGCTTC 1140
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QY 421 TGCGGCGCGCTCGCGCGCGCGTCTTGGTCAACCGGCGCGGCTCGCGCGCTCATCGCT 480
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QY 481 GTGCTCTGGGCGGTGCGGCTGTCTCTGCGGCTCTTGTTCCTGCTGGGCGGTGAG 540
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QY 541 CAGGACCCCGGATCTCCGTAGTCCGGGCGCTCAATGGCAACCGCGGATCGCTCCCTCG 600
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QY 601 CTTCTGCTCTGCTGCGCGCTCTCTGCTCTCTGCGGCGCGGCTCGCGGCGCTCG 660
Db 601 CTTCTGCTCTGCTGCGCGCTCTCTGCTCTCTGCGGCGCGGCTCGCGGCGCTCG 660
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Db 661 GGGCGGAGACCGGAGCGCGGCTGTTCAGCGCGGATGCGGCGGAGCGCGCGG 720
QY 721 CAGCTGGGCGGCTGCTGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 780
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QY 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGAGCAGCGCGGCGG 840
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGCGGAGCTGTGAGCAGCGCGGCGG 840
QY 841 CTGCGAGGCGCGCGCTCGGGCGGAGAGGAGCGGAGCGGAGCGGAGCGGAGCGG 900
Db 841 CTGCGAGGCGCGCGCTCGGGCGGAGAGGAGCGGAGCGGAGCGGAGCGGAGCGG 900
QY 901 C 901
Db 901 C 901

RESULT 7
US-09-876-252-129
; Sequence 129, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Re
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 129
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-876-252-129

Query Match 72.3%; Score 896.2; DB 10; Length 2040;
Best Local Similarity 99.7%; Pred. No. 6.4e-234;
Matches 898; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGGAGAGCCCTGGAAACGGCAGGAGCGCCCGAGGGGCGCGGAGCGCCCGTGGCC 60
Db 1 ATGGGAGAGCCCTGGAAACGGCAGGAGCGCCCGAGGGGCGCGGAGCGCCCGTGGCC 60
QY 61 GCGCTGCGGCTTTCGACAGCGCGCTGTCTGCGCCCTTTCCTGCGGGGCGCTGGTCCG 120
Db 61 GCGCTGCGGCTTTCGACAGCGCGCTGTCTGCGCCCTTTCCTGCGGGGCGCTGGTCCG 120
QY 121 GTGACCGCTGTGTCCTGTGTCCTGTCTGTCGTGTCGTGTCGTGTCGTGTCGTG 180
Db 121 GTGACCGCTGTGTCCTGTGTCCTGTCTGTCGTGTCGTGTCGTGTCGTGTCGTG 180
QY 181 ATGCTGATCGGGCGCTACCGGGACATCGGACACACCAACTGTACTCTGGGAGCATG 240
Db 181 ATGCTGATCGGGCGCTACCGGGACATCGGACACACCAACTGTACTCTGGGAGCATG 240
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QY 721 CAGCTGGGCGGCTCGTGTGATGCTGGGTACACCGGCTACTTCTTCTGCCCCCTT 780
Db 721 CAGCTGGGCGGCTCGTGTGATGCTGGGTACACCGGCTACTTCTTCTGCCCCCTT 780
QY 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCGG 840
Db 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCGG 840
QY 841 CTGGAGGCGGCGGCTCGGGCGGAGAGAGGCGCACCGGACAGCGTCCGGTCTG 900
Db 841 CTGGAGGCGGCGGCTCGGGCGGAGAGAGGCGCACCGGACAGCGTCCGGTCTG 900
QY 901 C 901
Db 901 C 901

RESULT 9

US-10-723-955-129
; Sequence 129, Application US/10723955
; Publication No. US20040110238A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lehman-Bruinsma, Karin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Gore, Martin
; APPLICANT: White, Carol
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US29.CON
; CURRENT APPLICATION NUMBER: US/10/723,955
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 10/417,820
; PRIOR FILING DATE: 2003-4-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-955-129

Query Match 72.3%; Score 896.2; DB 18; Length 2040;
Best Local Similarity 99.7%; Pred. No. 6.4e-234;
Matches 898; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGGAGCCCTTGGAGCGGACCGGCGGAGAGGCGGCGGAGCGGCGGCGGCGGCGG 60

Db 1 ATGGGAGCCCTTGGAGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
QY 61 GCGTGGCGGCTTCCGAGCGGCGGCTGCTCGGCCCTTTCCCTTGGGGGCGCTGCTGCGG 120
Db 61 GCGTGGCGGCTTCCGAGCGGCGGCTGCTCGGCCCTTTCCCTTGGGGGCGCTGCTGCGG 120
QY 121 GTGACCGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 GTGACCGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 ATGTGATTCGGGCGCTACCGGAGCATGCGGAGCACCACCACTTTGTACCTGGGCGAG 240
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QY 241 GCGGTGTCGACCTACTCATCTGCTGCGGCGCTGCGGCTGCGGCTGCGGCTGCGGCG 300
Db 241 GCGGTGTCGACCTACTCATCTGCTGCGGCGCTGCGGCTGCGGCTGCGGCTGCGGCG 300
QY 301 TCGGCGGCTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TCGGCGGCTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 TCGACCTAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 TCGACCTAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 TCGGCGGCTTCCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 TCGGCGGCTTCCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 GTGCTCTGGGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 481 GTGCTCTGGGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 CAGGACCCCGGCTTCCGAGTCCGCGGCTCAATGGCACCGGCGGATCGCCTTCCTCG 600
Db 541 CAGGACCCCGGCTTCCGAGTCCGCGGCTCAATGGCACCGGCGGATCGCCTTCCTCG 600
QY 601 CCTCTCGGCTCGGCGGCTTCCGAGTCCGCGGCTCAATGGCACCGGCGGATCGCCTTCCT 660
Db 601 CCTCTCGGCTCGGCGGCTTCCGAGTCCGCGGCTCAATGGCACCGGCGGATCGCCTTCCT 660
QY 661 GGGCGGAGACCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 GGGCGGAGACCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 CAGTGGGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 CAGTGGGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGGCGGCGG 840
Db 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGGCGGCGG 840
QY 841 CTGGAGGCGGCGGCTCGGGCGGAGAGAGGCGCACCGGCGAGACCGTCCGGTCTG 900
Db 841 CTGGAGGCGGCGGCTCGGGCGGAGAGAGGCGCACCGGCGAGACCGTCCGGTCTG 900
QY 901 C 901
Db 901 C 901

RESULT 10

US-10-417-820A-151
; Sequence 151, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.

Query Match	71.9%;	Score 891.4;	DB 17;	Length 2040;
Best Local Similarity	98.8%;	Pred. No. 1.3e-232;		
Matches 898;	Conservative 0;	Mismatches 11;	Indels 0;	Gaps 0
1	ATGGGACGCCCTGTGAAACGGACAGCAGCAGCCGAGGGGGCGCGAGCGCCGCGGCCC	60		
1	ATGGGACGCCCTGTGAAACGGACAGCAGCAGCCGAGGGGGCGCGAGCGCCGCGGCCC	60		
61	GGCGTGC CGCCTTGGACGAGCGCGCTGCTCGCCCTTTCCCTCGGGGCGCTGTGTGCGG	120		
61	GGCGTGC CGCCTTGGACGAGCGCGCGCTGCTCGCCCTTTCCCTCGGGGCGCTGTGTGCGG	120		
121	GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	180		
121	GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	180		
181	ATGCTGATCGGCGCGCTACCGGGACATGCGGACACACCACTCTGCTACTCGGGCAGCATG	240		
181	ATGCTGATCGGCGCGCTACCGGGACATGCGGACACACCACTCTGCTACTCGGGCAGCATG	240		
241	GC CGTGTCCGACCTACTCATCTGCTCGGGCTGCGGCTTCGACCTGTACCGCTCTCGGGCG	300		
241	GC CGTGTCCGACCTACTCATATGCTCGGGCTGCGGCTTCGACCTGTACCGCTCTCGGGCG	300		
301	TGCGGCGCTCGGGTGTTCGGGCGCTGCTCTGCGCGCTGTTCCTCTACGTGGGCGAGGCG	360		
301	TGCGGCGCTCGGGTGTTCGGGCGCTGCTCTGCGCGCTGTTCCTCTACGTGGGCGAGGCG	360		
361	TGCACCTACGCCACGCTGCTGACATGACCGGCGCTACCGGCTCAGCGGTCTACTCGGCCATC	420		
361	TGCACCTACGCCACGCTGCTGACATGACCGGCGCTACCGGCTCAGCGGTCTACTCGGCCATC	420		
421	TGCGCGCCGCTCGGGCGCGCTCTTGTGTACCCCGCGCGCGCTCGGGCGCTCATCGCT	480		
421	TGCGCGCCGCTCGGGCGCGCTCTTGTGTACCCCGCGCGCGCTCGGGCGCTCATCGCT	480		
481	GTGCTGTGGGCGGTGGCGGTGCTCTGTGCGGTTCCTTTGTTCTGTGTGGGCGGTCTGAG	540		
481	GTGCTGTGGGCGGTGGCGGTGCTCTGTGCGGTTCCTTTGTTCTGTGTGGGCGGTCTGAG	540		

Db 738 ATAACAACCCCTAAAGAGACGACGCGCCCGGAAAAAAGCGGAAACCGCGTAACCC 679
Qy 61 GCGCTGCGCCCTTGGAGAGCGCGCTGCTCGCCCTTTCCCTCGGGCGCTGCTGCGC 120
Db 678 GCGCTACCGCTTACGAGAAAGCGCGTACTCGCCCTTTCCCTTAAACGCTAATACG 619
Qy 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 180
Db 618 ATAACCGCTATATACCTATACCTATATATGCTGTGCTGTGCTGTGCTGTGCTGT 559
Qy 181 ATGCTGATCGGCGCTACCGGAGCATGCGGACCAACCACTTCTGCTGTGCTGTGCTG 240
Db 558 ATACTAATGAACGCTACCGAAACATACGAAACCACTTATATATATATATATAT 499
Qy 241 GCGGTGTGCGACCTACTCATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCG 300
Db 498 ACGGTATCGACCTACTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 439
Qy 301 TCGGCGCCCTGCGGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 438 TCGGACCCCTAAATATTCGAAACGCTACTCTACCGCTATCTACCGCTATCTACCG 379
Qy 361 TGCACCTAGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 378 TACACCTAGCCACGCTACTACACATACCGGCTCAACGCTGCAACGCTTAAACCAT 319
Qy 421 TCGCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 318 TACCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 259
Qy 481 GTGCTGTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 258 ATACTTAAACGCTAAGCTACTCTCTACCGTATCTCTTATCTTAAACGCTGAA 199
Qy 541 CAGACCCCGCATCTCGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 198 CAAACCCCGCATCTCGCTAATACCGAAACCTCAATACCGCGCGAATCGCTCTCG 139
Qy 601 CCTCTGCTGCTGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 138 CTTCTGCTGCTGCGCGCTCTCTTAACTCTGCGAAACCGCACCGCGCTGCTGCTGCT 79
Qy 661 GGGCCCGAGACCGCGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 78 AAACCGGAAACCGGAAACCGGAGCTATTCAACCGGAAATACCGACCGAACCGCGG 19
Qy 721 CAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 738
Db 18 CAACTAAACGCGCTAGCT 1

RESULT 14

US-10-363-483A-33738
; Sequence 33738, Application US/10363483A
; Publication No. US2005006401A1
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses

; FILE REFERENCE: 82011

; CURRENT APPLICATION NUMBER: US/10/363,483A

; CURRENT FILING DATE: 2003-03-03

; NUMBER OF SEQ ID NOS: 40712

; SEQ ID NO 33738

; LENGTH: 1179

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

; OTHER INFORMATION: CpG-island No: 33738

US-10-363-483A-33738

Query Match 40.5%; Score 501.2; DB 19; Length 1179;
Best Local Similarity 79.9%; Pred. No. 2.5e-126;
Matches 590; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 1 ATGGGCGACCCCTGGAACGGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Db 442 ATAAACAAACCCCTAAAGAGACGACGCGCCCGGAAAAAAGCGGAAACCGCGTAACCC 501
Qy 61 GCGGTGCGCGCTTGGAGAGCGCGCTGCTCGCCCTTTCCCTCGGGCGCTGCTGCGC 120
Db 502 GCGTACCGCTTACGAGAAAGCGCGTACTCGCCCTTTCCCTTAAACGCTAATACG 561
Qy 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 180
Db 562 ATAACCGCTATATACCTATACCTATATGCTGTGCTGTGCTGTGCTGTGCTGTGCT 621
Qy 181 ATGCTGATCGGCGCTACCGGAGCATGCGGACCAACCACTTGTAGCTGGGAGCATG 240
Db 622 ATACTAATCGAACGCTACCGAAACATACGAAACCACTTATATATATATATATAT 681
Qy 241 GCGGTGCGGACCTACTCATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCG 300
Db 682 ACGGTATCGACCTACTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
Qy 301 TCGGCGCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 742 TCGGACCCCTAAATATTCGAAACGCTACTCTACCGCTATCTCTTAAACGAAAC 801
Qy 361 TGCACCTAGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 802 TACACCTAGCCACGCTACTACACATACCGGCTCAACGCTGCAACGCTTAAACCAT 861
Qy 421 TCGCGCGCGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 862 TACCGCGCGCTCGCGCGCGCTGCTTAACTCTACCGCGCGCTGCTGCTGCTGCTGCT 921
Qy 481 GTGCTGTGCGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 922 ATACTTAAACGCTAAGCTACTCTCTACCGTATCTCTTATCTTAAACGCTGAA 981
Qy 541 CAGACCCCGCATCTCGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 982 CAAACCCCGCATCTCGCTAATACCGAAACCTCAATACCGCGCGAATCGCTCTCG 1041
Qy 601 CCTCTGCTGCTGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 1042 CTTCTGCTGCTGCGCGCTCTCTTAACTCTGCGAAACCGCACCGCGCTGCTGCTGCT 1101
Qy 661 GGGCCCGAGACCGCGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 1102 AAACCGGAAACCGGAAACCGGAGCTATTCAACCGGAAATACCGACCGAACCCGCG 1161
Qy 721 CAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 738
Db 1162 CAACTAAACGCGCTAGCT 1179

RESULT 15

US-10-363-345A-33739

; Sequence 33739, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Method for determining the degree of methylation of defined

; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3

; FILE REFERENCE: E01/1227

; CURRENT APPLICATION NUMBER: US/10/363,345A

; CURRENT FILING DATE: 2003-03-03

; NUMBER OF SEQ ID NOS: 40712

; SEQ ID NO 33739

```
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 33739
US-10-363-345A-33739

Query Match          35.3%; Score 437.2; DB 18; Length 1179;
Best Local Similarity 74.5%; Pred. No. 6.8e-109;
Matches 550; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 1 ATGGGCAGCCCTGGAAACGGCAGACGCGCCCGAGGGGGCGGAGCCGCCCGTGGCCC 60
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
442 ATGGGTAGTTTTTGGAAACGGTAGCATCGTTTCGAGGGGGCGGAGTCTGCTGGTTC 501
QY 61 GCGCTGCCGCCCTTGGCAGAGCGCGCTGCTGCCCTTTCCCTCGGGGGCGCTGGTCCG 120
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
502 GCGTTGTCGTTTTGGCAGAGCGTCGTTGTTCTGTTTTTTTTTGGGGCGCTGGTTCG 561
QY 121 GTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
562 GTGATCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 621
QY 181 ATGCTGATCGGCGCTACCGGACATGCGGACACCACTTGTACTGTGGCAGCATG 240
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
622 ATGTTGATCGGGCGTTATCGGATATCGGATTATTATTATTGTTATTGGGTAGTAG 681
QY 241 GCGGTGTCGACCTACTCATCTGCTCGGGCTGCCGTTTCGACCTGTACCGCTCTGGCGC 300
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
682 GTCGTGTTTCGATTATTATTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 741
QY 301 TCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
742 TCGCGGTTTTGGGTGTTGGGTGTTGGGTGTTGGGTGTTGGGTGTTGGGTGTTGG 801
QY 361 TGCACCTAGCCACACGCTGTCACATGACCGGCTCAGCGTCGAGCGTACCTGGCCATC 420
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
802 TGTATTACGTTACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 861
QY 421 TCCCGCGCGCTCCGCGCGCGCTCTTGGTCACCGCGCGCGCGCTCCGCGCGCTCATCGCT 480
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
862 TGTCTGCTGTTTCGGGTTTCGGGTTTGGTTTATTCGGCGTTCGGCGCTTTATCGTT 921
QY 481 GTGCTCTGGGCGTGGCGCTGCTCTGCGGTCCTCTTCTTCTGTTCTGTTGGGTCGAG 540
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
922 GTGTTTGGGTCGTGGCGGTTGTTTGTGCGGTTTTTTTTTGTGTTGGTGGGCGTCGAG 981
QY 541 CAGGACCCCGGATCTCCGTAGTCCCGGCTCAATGGCACCGCGCGGATCGCCTCTCTCG 600
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
982 TAGGATTCGGTATTTTCGTAGTTTCGGTTTTTAATGTTATCGCGCGGATCGTTTTTCG 1041
QY 601 CCTCTCGGCTCTGTCGCGGCTCTGCGCTCTGCGGCGGCGGCGGCGGCGGCGGCG 660
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1042 TTTTTCGTTTCGTCGCTGTTTTTTTGGTTTTTCGCGGCGGTTATCGCTGTTTCGTCGTCG 1101
QY 661 GGGCCCGGAGACCGGAGCGCGGCGCTGTTTCAGCCGGAATCGCGCGAGCCCGCGCG 720
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1102 GGGTTCGAGATCGCGAGGTCGCGGCGTTGTTAGTCGCGAATGTCGTCGAGTTTCGCG 1161
QY 721 CAGCTGGGCGGCTCGCT 738
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1162 TAGTTGGGCGGTTGCGT 1179
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Query Match 18.7%; Score 231.6; DB 9; Length 1046;
Best Local Similarity 68.8%; Pred. NO. 1.8e-39;
Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 92 CGCCCTTTCCTTGGGGCGCTGTGTCGGGTACCGCTGTGCTGTGCTGTTCCTTCGTG 151

Db 55 CACTGTTCCCGCGCGCTGCTGCGCGGCGTCACTGCCACCTGCGTGGCGCTCTTCGTGG 114

Qy 152 TCGGGGTGAGCGGCAACCTGTGTGACCGTGTGCTGATCGGGCGCTACCGGACATCGCGA 211

Db 115 TGGGCATCTCGGGCAACCTGTGTGACCGTGTGCTGATCGGGCGCTACCGGACATCGCGA 174

Qy 212 CCACCACCAACTTGTACCTGGCGACATGCGCGTGTGCGACCTACTCATCTGCTCGCGG 271

Db 175 CCACCACCAACTTGTACCTGGCGACATGCGCGTGTGCGACCTACTCATCTGCTCGCGG 234

Qy 272 TGCCTTTCGACTGTACCGCTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCTCT 331

Db 235 TGCCTTTCGACTGTACCGCTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCTCT 294

Qy 332 GCGCGCTGCTTACCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 391

Db 295 GCAAACTCTTCCAGTTTGTACGAGAGAGTGCACCTACGCCACGGTCTCCACCATCACCG 354

Qy 392 CGCTCAGCGTGCAGCGCTACCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 451

Db 355 CGCTCAGCGTGCAGCGCTACCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 414

Qy 452 CCGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 511

Db 415 CCAAGGCGCGTGTGAAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCGCG 474

Qy 512 GTCCCTTCTTGTCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 553

Db 475 GCGCCATCTTCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 516

RESULT 2

AK049671
LOCUS Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
DEFINITION enriched library, clone:CS30020122 product:GROWTH HORMONE
SECRETAGOGUE RECEPTOR TYPE 1 homolog [Rattus norvegicus], full
insert sequence.

AK049671
VERSION AK049671.1 GI:26340405
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kusunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

AUTHORS

TITLE

JOURNAL

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JOURNAL

REFERENCE

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5

The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 4435)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

Location/Qualifiers
1. 4435
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM:DB:CS30020122"
/db_xref="taxon:10090"
/clone="CS30020122"
/tissue_type="spinal cord"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
252..1346

/note="unnamed protein product; GROWTH HORMONE
SECRETAGOGUE RECEPTOR TYPE 1 homolog [Rattus norvegicus]
(SWISSPROT|O08725, evidence: FASTA, 99.5%id, 100%length,
match=1092)
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/codon_start=1
/protein_id="BAC33866.1"
/db_xref="GI:26340406"

Query Match 18.6%; Score 230; DB 3; Length 4435;
Best Local Similarity 68.6%; Pred. No. 4.4e-39;
Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

92 CGCCCTTCCCTGGGGCGCTGTCGCGGTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 151

Db 355 CACTGTTCCCGCGCGTCTGCGGGCGGTGCTGACCTGCGTGGGGCTTTCGTGG 414
Qy 152 TCGGGGTGAGCGGCAACGCTGTGACCGTGTGATCGGGCGCTACCGGACATGCGGA 211
Db 415 TGGGCATCTCGGGCAACGCTGTGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 474
Qy 212 CCACACCACTTGTACCTGCGGCGAGTGGCGGCTGCGACCTACTATCTGCTGCGGC 271
Db 475 CCACACCACTTGTACCTGCGGCGAGTGGCGGCTGCGACCTACTATCTGCTGCTGCTG 534
Qy 272 TCGCGGTGAGCTGTACCGCTGCTGCGGCTGCGGCGCTGCGGCTGCGGCTGCTGCT 331
Db 535 TCGCGGTGAGCTGTGCGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCTGCTGCT 594
Qy 332 GCGCGCTGTCTTACGCTGCGGCGAGGCTGACCTAGCCACGCTGCTGACATGACCG 391
Db 595 GCAACTCTTCCAGTTTGTGAGGAGAGTGTGACCTAGCCACGCTGCTGACATGACCG 654
Qy 392 CGCTCAGGCTGAGCGCTGTGCGGCTGCTGCGGCGCTGCGGCGCTGCGGCTGCTGCTG 451
Db 655 CGCTCAGGCTGAGCGCTGTGCGGCTGCTGCGGCGCTGCGGCGCTGCGGCTGCTGCTG 714
Qy 452 CCGGCGCGGCTGCGGCGCTGCTGCGGCTGCTGCGGCGCTGCGGCGCTGCTGCTGCGG 511
Db 715 CCAAGGCGGCTGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774
Qy 512 GTCCCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
Db 775 GCGCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816

RESULT 3
CO959476 688 bp mRNA linear EST 17-AUG-2004
LOCUS AGENCOURT_30842629 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE:7389798 5', mRNA sequence.

CO959476
VERSION CO959476.1 GI:51324050
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: c9apbs-r@mail.nih.gov

Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB18 row: c column: 04
High quality sequence stop: 170.
Location/Qualifiers

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7389798"
/tissue_type="mixed"
/lab_host="DH10B (T1-phase-resistant)"
/clone_lib="NIH MGC 146"
/note="Vector: pcDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or

from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pcDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image/rearrayed_plates/IRBF.presv.dat
a. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 18.4%; Score 228.4; DB 7; Length 688;
Best Local Similarity 79.8%; Pred. No. 8.e-39;
Matches 265; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
Qy 1 ATGGGAGCCCTGTGAACGAGGACGCGCCCGGAGGGGGCGGAGCGCCGCTGGGCC 60
Db 3 ATGGGAGCCCTGTGAACGAGGACGCGCCCGGAGGGGGCGGAGCGCCGCTGGGCC 62
Qy 61 GCGTGGCGGCTTGGAGGAGGCGCTGCTGCGGCTTCCCTGGGGGCGCTGCTGGCG 120
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Qy 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 123 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 182
Qy 181 ATGCTGATCGGGCGCTACCGGAGCATGCGGACCAACCACTTGTGTAATCTGGGAGCATG 240
Db 183 TTGTTGCTCTGGCGCTGTGCGGNGTGTGGGGCTCTTCTCTGCTTGGCCCTGGGGCGCG 242
Qy 241 GCGTGGCGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 243 TGGGTGCTCTGNNGTCTCTCCCGGTTGNGCGNGGTGGCGGCTTTCGCCCCCTGGCTC 302
Qy 301 TCGCGGCGCTGGGTGCTTCCGGCGCTGCTGCTG 332
Db 303 TCGTGGGCTGTTGTTCCCGGTGTGCTTGG 334

RESULT 4

CD618070/c
LOCUS CD618070 640 bp mRNA linear EST 12-JAN-2004
DEFINITION 56030361H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD618070
VERSION CD618070.1 GI:40266335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES

source
Location/Qualifiers
1..640
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 18.4%; Score 227.8; DB 6; Length 640;
Best Local Similarity 68.3%; Pred. No. 1.2e-38;
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;
Qy 93 GCCCTTTCCCTGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 152

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481 GCTCTTCCCGCGCGTCTGCGCGCGTACAGCCACCTGCGTGGCACTCTTCGTGT 422
153 CGGGGTAGCGCAACGTTGACCGTGTATGCTGATCGGGGCTACCGGGAATCGGAC 212
421 GGGTATCGTGGCAACCTGCTCACCATGCTGGTGTGTCGCGCTTCCGCGAGCTCGCAC 362
213 CACCAACCACTGTACCTGGGAGATGCGCGTGTCCGACCTACTCATCTGCTCGGCT 272
361 CACCAACCACTGTACCTGGGAGATGCGCGTGTCCGACCTACTCATCTGCTCGGCT 302
273 GCGGTTCGACCTGTACCGCTCTGCGGCTCGCGGCTGTGGTGTTCGGGCGCTGCTCTG 332
301 GCGGTTCGACCTGTACCGCTCTGCGGCTCGCGGCTGTGGTGTTCGGGCGCTGCTCTG 242
333 CGCGTGTCTCTAGTGGGAGGCTGACCTACCGGCTGTGGTGTTCGGGCGCTGCTCTG 392
241 CAAACTCTTCCAACTTCCGAGTGTGAGTGTGACCTACCGGCTGTGGTGTTCGGGCG 182
393 GCTCAGCGTGGAGGCTACCTGCGCATCTGCGGCTGTGGGCTGTGGTGTTCGGGCG 452
181 GCTGAGCGTGGAGGCTACCTGCGCATCTGCGGCTGTGGGCTGTGGTGTTCGGGCG 122
453 CGCGGCGCGGCTGTGGGCTGTGGTGTGTCTGCGGCTGTGGGCTGTGGTGTTCGGGCG 512
121 CAAAGGGGCGGTGAAGTGTGTCTCTGTCATCTGCGGCTGTGGGCTGTGGGCGCGG 62
513 TCCCTTCTTGTCTGCGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTATC 555
61 GCCCATCTTCTGCTAGTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTATC 19

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RESULT 5
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LOCUS 56030361J1 FLP Homo sapiens cDNA, mRNA linear EST 12-JAN-2004
ACCESSION CD618071
VERSION CD618071.1 GI:40266336
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 640)
Fu G.K., Wang J.T., Yang J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1..640
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="Vector: pDrive Cloning Vector"
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Query Match 18.4%; Score 227.8; DB 6; Length 640;
Best Local Similarity 68.3%; Pred. No. 1.2e-38;
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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93 GCCCTTCCCTGGGGCGCTGTGCGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 152
157 GCTCTTCCCGCGCGCTGCTGCGGCGCTGTGCGGCGCTGTGCGGCGCTGTGCGGCGCTGTGCGGCT 216
153 CGGGGTAGCGCAACGTTGACCGTGTATGCTGATCGGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 212
217 GGGTATCGTGGCAACCTGCTCACCATGCTGGTGTGTCGCGCTTCCGCGAGCTCGCAC 276

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213 CACCACCAACTTGTACCTGGGAGATGCGCGTGTCCGACCTACTCATCTGCTCGGCT 272
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337 GCGGTTCGACCTGTGCTCGCTTGGAGTACCGGCTGTGGAACTTTCGGGCGACCTCTCTG 396
333 CGCGTGTCTCTAGTGGGAGGCTGTGACCTACCGGCTGTGGTGTTCGGGCGCTGCTGACATGACGCG 392
397 CAAACTCTTCCAACTTCCGAGTGTGAGTGTGACCTACCGGCTGTGGTGTTCGGGCGCTGCTCATCAGC 456
393 GCTCAGCGTGGAGGCTACCTGCGCATCTGCGGCTGTGGGCTGTGGGCTGTGGTGTTCGGGCGCTGCTCATC 452
457 GCTGAGCGTGGAGGCTACCTGCGCATCTGCGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTCATC 516
453 CGCGGCGCGGCTCGCGGCTCATGCTGTGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTATC 512
517 CAAAGGGGCGGTGAAGTGTGTCTCTGTCATCTGCGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTATC 576
513 TCCCTTCTTGTCTGCGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTATC 555
577 GCCCATCTTCTGCTAGTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTATC 619

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RESULT 6
AY407664
LOCUS Homo sapiens GHR gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY407664
VERSION AY407664.1 GI:39763635
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1052)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1..1052
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/gene="GHR"
/locus_tag="HCM2966"
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Query Match 18.4%; Score 227.8; DB 9; Length 1052;
Best Local Similarity 68.3%; Pred. No. 1.2e-38;
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;
93 GCCCTTCCCTGGGGCGCTGTGCGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 152

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PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCACGAG
 Plats: 49 Row: I Column: 6
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 Location/Qualifiers
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Source
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Location/Qualifiers
1ncvte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@ncvte.com.
/organism="Homo sapiens"
/mol_type="mRNA"
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FLC I."

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/locus_tag="HCM2966"

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		Best Local Similarity		56.3%; Pred. No. 1.4e-35;	
		Matches 293; Conservative 0; Mismatches 124; Indels 0; Gaps 0;		Matches 562; Conservative 0; Mismatches 308; Indels 129; Gaps 4;	
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DB	2	TGGCGCTCTTCGTGGGTCATCTCGGCAACCTGCTACCATGCTGGTGTCCCGCT	61		
QY	197	ACCGGACATCGGACCCACCACTTGTACCTGGGAGCATGCCGTGTCGACCTAC	256		
DB	62	TCGGGAGTGGGACCCACCACTTGTACCTGGGAGCATGCCGTGTCGACCTAC	121		
QY	257	TCATCTGTTCGGGCTGCGGCTTCGACCTGTACCGCTCTGGGCTTCGGGCTTCGGGCT	316		
DB	122	TCATCTGTTCGGGCTGCGGCTTCGACCTGTACCGCTCTGGGCTTCGGGCTTCGGGCT	181		
QY	317	TGGGCGGTGTCTGCGGCTGTCCCTCTACGTGGGAGGGTGCACCTACGACGCG	376		
DB	182	TGGGCGGTGTCTGCGGCTGTCCCTCTACGTGGGAGGGTGCACCTACGACGCG	241		
QY	377	TGCTGCATGACCGGCTCAGCGTGTACGCTGTACGCTGTCCCTCTACGCTGTGGGCGG	436		
DB	242	TGCTGCATGACCGGCTCAGCGTGTACGCTGTACGCTGTCCCTCTACGCTGTGGGCGG	301		
QY	437	CCCGGCTGTTCGTACCGGCGCGGCTCGGCGCTCATCGCTGTCTGGGCGGCTGG	496		
DB	302	CCAGGTGGTGTACCAAGGCGGCTGTGAAGCTGTTCATCTTGGGCGGCTGG	361		
QY	497	CGCTGTCTTCGCGGCTCCCTTCTTGTCTTCGCTGGGCGGTGAGCAGACCCCGCA	553		
DB	362	CCTTCTGAGCGCGGCGGCTTCCTGCTGCTGGTGGGCGGTGAGCAGACCGCA	418		

RESULT 10
AY407665
LOCUS
DEFINITION
Pan troglodytes GHSR gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY407665
VERSION
AY407665.1
KEYWORDS
GI:39763636
ORGANISM
Pan troglodytes (chimpanzee)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 969)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1..969
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>969
gene

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2778 row: p column: 05
High quality sequence stop: 534.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6577973"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 15.0%; Score 186.4; DB 5; Length 843;
Best Local Similarity 91.0%; Pred. No. 1e-29;
Matches 243; Conservative 0; Mismatches 17; Indels 7; Gaps 4;
QY 906 GGTGGTCTTGGCATTATTAATTTGGTGTGGCTTCCAGTGGCAGAAATCAATTTACAT 965
DB 534 GGTGGTCTTGGCATTATTAATTTGGTGTGGCTTCCAGTGGCAGAAATCAATTTACAT 593
QY 966 AACACGGAGATTCGGGATGATGTACTTCTCTGACTACTTTAAACATCGTCGCTCTGCA 1025
DB 594 AACACGGAGATTCGGGATGATGTACTTCTCTGACTACTTTAAACATCGTCGCTCTGCA 653
QY 1026 ACTTTTCTACTGAGGGCATCTATCAACCAATCTCTTCAACCTC-ATTTCAAAGAAGT 1084
DB 654 ACTTTTCTACTGAGGGCATCTATCAACCAATCTCTTCAACCTCAATTTCAAGAGT 713
QY 1085 AC-AGAGCGCGCGCTTTAAA-----CTGTGCTGCGAAGGAAGTCCAGCGCAG-AGGCT 1138
DB 714 ACAAGAGCGCGCGCTTTAAACTGTCTGTCGAGGGAAGTCCCAGCGCAGAGGCT 773
QY 1139 TCCACAGACGAGGACATCGCGGGG 1165
DB 774 CCCACAGACGAGGACATCGCGGGG 800

RESULT 15
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LOCUS 56030445J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD618075
ACCESSION CD618075.1 GI:40266340
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 635)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)

REFERENCE
AUTHORS
TITLE
JOURNAL

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2005, 12:58:01 ; Search time 68.6667 Seconds
(without alignments)
2320.562 Million cell updates/sec

Title: US-09-719-485-3
Perfect score: 2155
Sequence: 1 MGSPWNGSDGEGAREPWP.....DTGDTGCVTETSANVTMG 412

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2155	100.0	412	3	AA54145 Amino aci
2	2155	100.0	412	4	AAB68478 Amino aci
3	2155	100.0	412	4	AAB62652 Long form
4	2155	100.0	412	5	ABG30936 Human G p
5	2155	100.0	412	6	ABP81993 Human mot
6	2155	100.0	412	8	ADN11761 Human mot
7	2155	100.0	412	8	ADO29697 Human GPC
8	2155	100.0	412	8	ADQ37921 Human G-p
9	2155	100.0	501	4	AAG65822 Human GPR
10	2149	99.7	412	3	AAB02854 Human G p
11	2149	99.7	412	8	ADG86491 Human hgp
12	2149	99.7	412	8	ADG86511 Human orp
13	2149	99.7	412	8	ADP20284 Human GPC
14	2141	99.4	412	5	ABB09535 Human mot
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17	1581	73.4	386	3	AA54146 Amino aci
18	1581	73.4	386	4	AAB62653 Short for
19	1581	73.4	386	8	ADN11763 Human mot
20	1149.5	53.3	271	4	AAB68476 Amino aci
21	907	42.1	363	3	AA54147 The puffe
22	907	42.1	363	4	AAB68479 Amino aci
23	865.5	40.2	349	3	AA169293 A canine
24	863.5	40.1	366	3	AA570345 Human G p
25	863.5	40.1	366	3	AA590632 Human G p

ALIGNMENTS

RESULT 1
AA54145
ID AA54145 standard; protein; 412 AA.

XX AA54145;

AC AA54145;

DT 27-MAR-2000 (first entry)

XX Amino acid sequence of the motilin receptor splice variant MTL-R1A.

XX Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;

KW spliced form; MTL-R1A; MTL-R1B; gastric motility disorder;

KW functional defect; neurological disorder; scleroderma; colonoscopy;

KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;

KW infection; stress-related motility disorder; psychogenic disorder;

KW gastroparesis; gastro-oesophageal reflux disease; constipation;

KW chronic idiopathic pseudo obstruction; acute faecal impaction;

KW postoperative ileus; gallstones; infantile colic; diarrhoea;

KW irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;

KW endoscopy; duodenal intubation.

OS Homo sapiens.

XX WO9964436-A1.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-US012773.

XX 12-JUN-1998; 98US-0089098P.

XX (MERI) MERCK & CO INC.

XX Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;

XX Pong S, Smith RG;

XX WPI; 2000-105868/09.

XX N-PSDB; AA245403.

XX Novel receptor protein for screening compounds used in treating irritable

XX bowel syndrome, constipation and other gastric conditions.

XX Claim 3; Fig 3; 44pp; English.

XX The present sequence represents splice variant MTL-R1A of the motilin

XX receptor. The gene encodes a G-protein coupled receptor, and is

XX designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A

XX (see AA54145) and MTL-R1B (see AA54146). MTL-R1A is a functional seven

XX

transmembrane domain form, and MTL-R1B is a truncated five transmembrane domain. The MTL-R1 proteins are used to identify agonists and antagonists which can be used for treating gastric motility disorders, functional defects, disorders secondary to neurological disorders e.g. scleroderma, paraneoplastic syndromes radiation induced dysmotility, diabetes, infections, stress-related motility disorders, psychogenic disorders, gastroparesis, gastro-oesophageal reflux disease, constipation, chronic idiopathic pseudo obstruction, acute faecal impaction, postoperative ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer dyspepsia, non-cardiac chest pain and diarrhoea. They can also be used in the preparation for colonoscopy, endoscopy and duodenal intubation

Sequence 412 AA;

Sequence 412 AA;

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Query Match      100.0%; Score 2155; DB 3; Length 412;
Best Local Similarity 100.0%; Pred. No. 3.8e-195;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	61	MLIGRYDMRTTNYL	LGSMVAVDLLILGLPFDYLWRSRPWWFGPLLCRLSLYVGE	120
Qy	121	CTYATLLHMTALS	VERYLAI CRPLRARVLVTRRRVRALI AVLWAVALLSAGFPFLVGVE	180
Db	121	CTYATLLHMTALS	VERYLAI CRPLRARVLVTRRRVRALI AVLWAVALLSAGFPFLVGVE	180
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Qy	301	LVVVLAFLICWLP	PHVGRIIYINTEDSRMVFSQYFNIVALQLFYLASINPILYNLISK	360
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RESULT 2

RECEIVED
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ID AAB68478 standard: protein: 412 AA.

AC AAB68478:

DT 23-JUL-2001 (first entry)

XX DE Amino acid sequence of a human motilin receptor polypeptide.

AA	Motilin receptor; gastrointestinal disease; gastric motility disorder;
KW	gastroparesis; irritable bowel syndrome; diarrhoea.
KW	

OS Homo sapiens.

AA
PN
WO200132710-A1.

XX
PD
10-MAY-2001.XX
PF 25-OCT-2000; 2000WO-US029426.

XX
PR 29-OCT-1999; 99US-0162264P.

PA (MERI) MERCK & CO INC.

Tan C, McKee K;

•

XX WPI: 2001-343479/36.
 DR N-PSDB; AAF85449.
 DR XX
 PT Novel polypeptides related to dog and rabbit motilin receptor
 PT polypeptide, comprising unique regions from dog and motilin receptor
 PT amino acid sequence, useful for identifying compounds for treating
 PT diarrhea in humans.
 XX
 PS Disclosure; Page 32-33; 42pp; English.
 PS

AA The present sequence represents a human motilin receptor polypeptide. The
 CC specification describes a unique sequence present in exon 1 of the dog
 CC motilin receptor, which is not present in human or *Sphaeroides nophilus*
 CC 7357 motilin receptor sequences. The unique nucleic acid sequence is
 CC useful for measuring the ability of a compound to affect motilin receptor
 CC activity. Motilin receptor polynucleotides and polypeptides are used to
 CC identify therapeutic compounds which are useful for treating
 CC gastrointestinal diseases and disorders such as gastric motility
 CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea
 XX
 SQ Sequence 412 AA;

Query Match	100.0.0%;	Score 2155;	DB 4;	Length 412;
Best Local Similarity	100.0.0%;	Pred. No. 3.8e-195;		
Matches 412;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGSPWNGSDGEGARBPWPALPCDBERRCSPPFLGALVPVTA	VCVLCCLFVVGSGNNVTV	60
Db	1	MGSPWNGSDGEGARBPWPALPCDBERRCSPPFLGALVPVTA	VCVLCCLFVVGSGNNVTV	60
Qy	61	MLIGRYDRMRTTNLYLGSMAVSDLLILGLPDLVRLWRSRP	PWVGPLLCLRLSLYVGG	120
Db	61	MLIGRYDRMRTTNLYLGSMAVSDLLILGLPDLVRLWRSRP	PWVGPLLCLRLSLYVGG	120
Qy	121	CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLTA	VLAVALSAGPFLVNGVE	180
Db	121	CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLTA	VLAVALSAGPFLVNGVE	180
Qy	181	QDPGISVVPGLNGTARIASSPPLMLSRAPPPSPGPGPTAA	AAALFSECRPSPA	240
Db	181	QDPGISVVPGLNGTARIASSPPLMLSRAPPPSPGPGPTAA	AAALFSECRPSPA	240
Qy	241	QLGALRVLMTWTAYFPFLPCLCLSLYGLIGRELWSRRPL	RGRPAASGRGRHQTVRL	300
Db	241	QLGALRVLMTWTAYFPFLPCLCLSLYGLIGRELWSRRPL	RGRPAASGRGRHQTVRL	300
Qy	301	LVVLAFFICWLPFHVGRITIIYINTDSRMVFSQYFNIVAL	QQLFYLSASINPLYNLISK	360
Db	301	LVVLAFFICWLPFHVGRITIIYINTDSRMVFSQYFNIVAL	QQLFYLSASINPLYNLISK	360
Qy	361	KYRAAFAKLLARKSRPRGPHRSRDTAGEVAGDTGDTGV	TYTSTSNVNTMG	412
Db	361	KYRAAFAKLLARKSRPRGPHRSRDTAGEVAGDTGDTGV	TYTSTSNVNTMG	412

RESULT 3

AAB62652
 ID AAB62652 standard: protein: 412 AA.

XX AAB62652:

XX
DT 23-JUL-2001 (first entry)

XX DE Long form of motilin receptor, GPR-38A isoform.

KW *zig33*; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
 KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38A; isoform
 OS
 OS Homo sapiens.
 OS

XX SQ Sequence 412 AA;
Query Match 100.0%; Score 2155; DB 5; Length 412;
Best Local Similarity 100.0%; Pred. No. 3.8e-195;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPGAREPPWALPPCDERRCSPPFLGALVPVTAVALCLFLVVGVSNNVTV 60
Db 1 MGSPWNGSDGPGAREPPWALPPCDERRCSPPFLGALVPVTAVALCLFLVVGVSNNVTV 60
QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWFGLLCRLSLYVGE 120
Db 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWFGLLCRLSLYVGE 120
QY 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180
Db 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180
QY 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
Db 181 QDPGISVVGGLNGTARIASSPPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRHRQTIVRL 300
Db 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRHRQTIVRL 300
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQFLVLSINPILYNLSK 360
Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQFLVLSINPILYNLSK 360
QY 361 KYRAAFAKLLILARKSRPRGHRSDTAGVAGDTGGDTGVGTYSANVKTWG 412
Db 361 KYRAAFAKLLILARKSRPRGHRSDTAGVAGDTGGDTGVGTYSANVKTWG 412

RESULT 5
ABP81993
ID ABP81993 standard; protein; 412 AA.
XX
AC ABP81993;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human motilin receptor GPR38 protein SEQ ID NO:473.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
FN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burner GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.

DR N-PSDB; ABZ42842.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (1) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42842 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 412 AA;

Query Match 100.0%; Score 2155; DB 6; Length 412;
Best Local Similarity 100.0%; Pred. No. 3.8e-195;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPGAREPPWALPPCDERRCSPPFLGALVPVTAVALCLFLVVGVSNNVTV 60
Db 1 MGSPWNGSDGPGAREPPWALPPCDERRCSPPFLGALVPVTAVALCLFLVVGVSNNVTV 60
QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWFGLLCRLSLYVGE 120
Db 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWFGLLCRLSLYVGE 120
QY 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180
Db 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180
QY 181 QDPGISVVGGLNGTARIASSPPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
Db 181 QDPGISVVGGLNGTARIASSPPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRHRQTIVRL 300
Db 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRHRQTIVRL 300
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQFLVLSINPILYNLSK 360
Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQFLVLSINPILYNLSK 360
QY 361 KYRAAFAKLLILARKSRPRGHRSDTAGVAGDTGGDTGVGTYSANVKTWG 412
Db 361 KYRAAFAKLLILARKSRPRGHRSDTAGVAGDTGGDTGVGTYSANVKTWG 412

RESULT 6
ADN11761
ID ADN11761 standard; protein; 412 AA.

XX ADN11761;
 XX 15-JUL-2004 (first entry)
 XX Human motilin receptor GPR-38A protein.
 XX human; zsig33; body weight; body mass; antibody; antagonist;
 KW gastrointestinal; antiinflammatory; antitumor; vulnerary;
 KW growth hormone secretagogue; GHS-R; peptide-antibody complex;
 KW motilin receptor.
 XX Homo sapiens.
 OS WO2004033645-A2.
 XX 22-APR-2004.
 XX 06-OCT-2003; 2003WO-US031804.
 XX 07-OCT-2002; 2002US-0416918P.
 XX (ZYMO) ZYMOGENETICS INC.
 PI Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;
 XX WPI; 2004-340913/31.
 DR N-PSDB; ADN11760.
 XX Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,
 PT inhibiting signal transduction in a cell expressing a growth hormone
 PT secretagogue receptor, or treating a metabolic disorder.
 XX Disclosure; Page 95-96; 100pp; English.
 XX The present invention relates to the use of a zsig33 peptide for forming
 CC a peptide-antibody complex, purifying a peptide, inhibiting signal
 CC transduction in a cell expressing a growth hormone secretagogue receptor
 CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite
 CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a
 CC mammal, or treating a metabolic disorder. The peptide is useful for
 CC forming a peptide-antibody complex, purifying a peptide, inhibiting
 CC signal transduction in a cell expressing a GHS-R, decreasing fat
 CC deposition in a mammal, suppressing the appetite of a mammal, inhibiting
 CC growth hormone secretion in pituitary cells of a mammal, or treating a
 CC metabolic disorder. The zsig33 polypeptides can be used to study
 CC proliferation or differentiation in stomach, lung, pituitary,
 CC hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,
 CC skeletal muscle or pancreas. They are also useful in delivering
 CC therapeutic agents. Zsig33 polypeptides, agonists and antagonists are
 CC also useful for promoting wound healing. The polypeptides, nucleic acids
 CC and antibodies are useful for diagnosing, treating or preventing
 CC disorders associated with gastric reflux, gastroparesis, modulation of
 CC secretion of pituitary hormones, including growth hormone, Crohn's
 CC disease, metabolic wasting, gastric ulcers, weight management, or
 CC degenerative disease. The present sequence is the human motilin receptor
 CC GPR38A protein shown in the exemplification of the invention.
 XX Sequence 412 AA;
 SQ
 Query Match 100.0%; Score 2155; DB 8; Length 412;
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSPWNGSDGPGAGRPWPALPPCDERRCSFPFLGALVPVTAACLCIFVGVSGNVTV 60
 DB 1 MGSPWNGSDGPGAGRPWPALPPCDERRCSFPFLGALVPVTAACLCIFVGVSGNVTV 60
 QY 61 MLIGYRDWRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVFGPLLCRLSLYVGEG 120
 DB 61 MLIGYRDWRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPVFGPLLCRLSLYVGEG 120
 QY 121 CTYATLLHMTALSVRYLAICRPLRVLVTRRRVRLALVLAVALLSAGPFLVLGVE 180

Db 121 CTYATLLHMTALSVRYLAICRPLRVLVTRRRVRLALVLAVALLSAGPFLVLGVE 180
 QY 181 QDPGISVVPGLNGTARIASSPLASPPPLWLSRAPPPSPPPETAATAAALFSRECRPSPA 240
 Db 181 QDPGISVVPGLNGTARIASSPLASPPPLWLSRAPPPSPPPETAATAAALFSRECRPSPA 240
 QY 241 QLGALRVMLWTTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300
 Db 241 QLGALRVMLWTTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300
 QY 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQFLYLSASINPILYNLSK 360
 Db 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQFLYLSASINPILYNLSK 360
 QY 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGTETYSANVKTWG 412
 Db 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGTETYSANVKTWG 412

RESULT 7
 ADO29697
 ID ADO29697 standard; protein; 412 AA.
 AC ADO29697;
 XX 29-JUL-2004 (first entry)
 XX Human GPCR GPR38, SEQ ID NO:799.
 XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
 KW cytosolic; antineoplastic; vasotropic; antidiabetic; antidiabetic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianemic; antiepileptic;
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW receptor.
 XX Homo sapiens.
 OS WO2004040000-A2.
 PN 13-MAY-2004.
 XX 09-SEP-2003; 2003WO-US028226.
 XX 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX (PRIM-) PRIMAL INC.
 XX Gaitanaris GA, Bergmann JB, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 XX WPI; 2004-390329/36.
 DR N-PSDB; ADO30072.
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX Claim 151; SEQ ID NO 799; 542pp; English.
 PS The invention relates to human and mouse G protein-coupled receptors
 CC

(GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridize to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases) and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 412 AA;

Query Match 100.0%; Score 2155; DB 8; Length 412;
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPPLGALVPVTAACLCFLVVGSGNVTV 60
 Db 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPPLGALVPVTAACLCFLVVGSGNVTV 60

QY 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPDLRLWRSRPWFGPLLCRLSLYVGE 120
 Db 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPDLRLWRSRPWFGPLLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVRYLAICRPLRLRVLTTRRRVRLIAVLWAVALLSAGPFLVGE 180
 Db 121 CTYATLLHMTALSVRYLAICRPLRLRVLTTRRRVRLIAVLWAVALLSAGPFLVGE 180

QY 181 QDPGISVVPGLNGTARIASPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
 Db 181 QDPGISVVPGLNGTARIASPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

QY 241 QLGLALRVMLVTTAVFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRCHRTVRL 300
 Db 241 QLGLALRVMLVTTAVFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRCHRTVRL 300

QY 301 LVVLAFFICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLSK 360
 Db 301 LVVLAFFICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLSK 360

QY 361 KYRAAFAKLLARKSRPGFHSRDTAGEVAGDTGGDTVGVTETSANVKTWG 412
 Db 361 KYRAAFAKLLARKSRPGFHSRDTAGEVAGDTGGDTVGVTETSANVKTWG 412

RESULT 8

ADQ37921

ID ADQ37921 standard; protein; 412 AA.

XX AC ADQ37921;

XX AC ADQ37921;

DT 23-SEP-2004 (first entry)

XX DE Human G-protein-coupled receptor 38 protein.
 XX KW antiparkinsonian; neuroprotective; nootropic; cardiovascular; cardiant;
 KW vasotropic; antiarteriosclerotic; nephrotropic; uropathic;
 KW urology disease; cardiovascular disease;
 KW peripheral nervous system disorder; central nervous system disorder;
 KW G-protein-coupled receptor 38; GPR38; Parkinson's disease;
 KW multiple sclerosis; dementia; myocardial infarction; ischemic disease;
 KW atherosclerosis; renal failure; glomerulopathy; urinary incontinence.
 XX OS Homo sapiens.
 XX WO2004057328-A2.
 XX 08-JUL-2004.
 XX 11-DEC-2003; 2003WO-EP014052.
 XX 23-DEC-2002; 2002EP-00028753.
 XX (FARB) BAYER HEALTHCARE AG.
 XX Golz S, Brueggemeier U, Summer H;
 PI WPI; 2004-543310/52.
 DR N-FSDB; ADQ37920.
 XX
 PT Screening therapeutic agents for use in treatment of urology diseases and
 PT cardiovascular diseases in a mammal, comprises contacting a test compound
 PT with G-protein-coupled receptor 38, and detecting binding.
 XX
 PS Disclosure; SEQ ID NO 2; 11pp; English.
 XX
 CC The invention relates to a method of screening (M1) for therapeutic
 CC agents useful in the treatment of a disease chosen from urology diseases,
 CC cardiovascular diseases and disorders of the peripheral and central
 CC nervous system in a mammal, comprises contacting a test compound with a G
 CC -protein-coupled receptor 38 (GPR38) polypeptide, and detecting binding
 CC of the test compound to the GPR38 polypeptide. (M1) is useful for
 CC screening therapeutic agents useful in the treatment of a disease chosen
 CC from urology diseases, cardiovascular diseases and disorders of the
 CC peripheral and central nervous system in a mammal, such as Parkinson's
 CC disease, multiple sclerosis, dementia, cardiovascular disorders such as
 CC myocardial infarction, ischemic diseases, atherosclerosis, and urological
 CC disorders such as acute or chronic renal failure, glomerulopathies, and
 CC urinary incontinence. This sequence corresponds to the human G-protein-
 CC coupled receptor 38.
 XX
 SQ Sequence 412 AA;

Query Match 100.0%; Score 2155; DB 8; Length 412;
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPPLGALVPVTAACLCFLVVGSGNVTV 60
 Db 1 MGSPWNGSDGEGAREPPWPALPPCDERRCSPPLGALVPVTAACLCFLVVGSGNVTV 60

QY 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPDLRLWRSRPWFGPLLCRLSLYVGE 120
 Db 61 MLIGRYDRMTTNNLYGSMVSDLLILGLPDLRLWRSRPWFGPLLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVRYLAICRPLRLRVLTTRRRVRLIAVLWAVALLSAGPFLVGE 180
 Db 121 CTYATLLHMTALSVRYLAICRPLRLRVLTTRRRVRLIAVLWAVALLSAGPFLVGE 180

QY 181 QDPGISVVPGLNGTARIASPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
 Db 181 QDPGISVVPGLNGTARIASPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

QY 241 QLGLALRVMLVTTAVFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRCHRTVRL 300
 Db 241 QLGLALRVMLVTTAVFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRCHRTVRL 300

Db 241 QLGALRVMLWTTAYFFLPFLCLSLYLIGRELWSSRRPLRGPAASGRERHRTQTVRVL 300
Qy 301 LVVLAFTICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLASINPILYNLISK 360
Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLASINPILYNLISK 360
Qy 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412
Db 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412

RESULT 9
AAG5822
ID AAG5822 standard; protein; 501 AA.
XX
AC AAG5822;
DT 30-JAN-2002 (first entry)
XX
DE Human GPR38 variant GPR38V polypeptide.
XX
KW GPR38V; variant; antibacterial; cytostatic; analgesic; antiaesthetic;
KW anti-Parkinsonian; hypotensive; hypotensive; antidiabetic; osteopathic;
KW antiallergic; antimigraine; neuroleptic; nootropic; anticonvulsant;
KW antiulcer; antiemetic; cardiant; vaccine; human.
XX
OS Homo sapiens.
XX
XX WO200164836-A2.
XX
PD 07-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006277.
XX
XX 01-MAR-2000; 2000US-00516315.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Elshourbagy N, Shabon U;
XX
XX WPI; 2001-638956/73.
XX
XX N-PSDB; AAI6989.
XX
XX New human GPR38V polypeptide and polynucleotide, useful for treating e.g.
XX bacterial, fungal, protozoal and viral infections, cancers or allergies,
XX as vaccines, and for identifying agonists and antagonists potentially
XX useful in therapy.
XX
XX Claim 1; Page 26; 32pp; English.
XX
XX This represents a human GPR38 variant (GPR38V) polypeptide. GPR38V can be
XX expressed by standard recombinant methodology. The polynucleotides and
XX polypeptides are used in the treatment of bacterial, fungal, protozoal
XX and viral infections, infections caused by HIV-1 or HIV-2, pain, cancers,
XX diabetes, obesity, anorexia, asthma, Parkinson's disease, acute heart
XX failure, hypertension, urinary retentions, osteoporosis, allergies,
XX ulcers, migraine, psychotic and neurological disorders, or dyskinesias.
XX They are also useful for identifying agonists and antagonists that are
XX potentially useful in therapy, as vaccines to induce immunological
XX response in a mammal. The polypeptides may also be used as immunogens to
XX produce antibodies immunospecific for the polypeptides, and to identify
XX membrane bound or soluble receptors

SQ Sequence 501 AA;
Query Match 100.0%; Score 2155; DB 4; Length 501;
Best Local Similarity 100.0%; Pred. No. 4.8e-195;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSPWNGSDGEGAREPPWALPPCDERRCSPPFLGALVPVTAIVCLFVVGSGNVVTV 60
Db 90 MGSPWNGSDGEGAREPPWALPPCDERRCSPPFLGALVPVTAIVCLFVVGSGNVVTV 149

Qy 61 MLICRYDRMTTNTLYLGSMVAVSDLLILGLPPDLRYLRSRPWPVPGPLLCRLSLYVGE 120
Db 150 MLICRYDRMTTNTLYLGSMVAVSDLLILGLPPDLRYLRSRPWPVPGPLLCRLSLYVGE 209
Qy 121 CTYATLHMTALSVERYLAIICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFLVGVE 180
Db 210 CTYATLHMTALSVERYLAIICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFLVGVE 269
Qy 181 QDPGISVVGINGLTARIASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSPA 240
Db 270 QDPGISVVGINGLTARIASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSPA 329
Qy 241 QLGALRVMLWTTAYFFLPFLCLSLYLIGRELWSSRRPLRGPAASGRERHRTQTVRVL 300
Db 330 QLGALRVMLWTTAYFFLPFLCLSLYLIGRELWSSRRPLRGPAASGRERHRTQTVRVL 389
Qy 301 LVVLAFTICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLASINPILYNLISK 360
Db 390 LVVLAFTICWLPFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLASINPILYNLISK 449
Qy 361 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412
Db 450 KYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGGDTVGYTETSANVKTWG 501

RESULT 10
AAB02854
ID AAB02854 standard; protein; 412 AA.
XX
AC AAB02854;
DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hGPR38 (V297K) protein SEQ ID NO:130.
XX
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO2000022131-A2.
XX
PD 20-APR-2000.
XX
XX 13-OCT-1999; 99WO-US024065.
XX
XX 13-OCT-1998; 98US-00170496.
XX 12-NOV-1998; 98US-0108029P.
XX 20-NOV-1998; 98US-0109213P.
XX 27-NOV-1998; 98US-0110060P.
XX 16-FEB-1999; 99US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 12-MAR-1999; 99US-0123944P.
XX 12-MAR-1999; 99US-0123945P.
XX 12-MAR-1999; 99US-0123946P.
XX 12-MAR-1999; 99US-0123948P.
XX 12-MAR-1999; 99US-0123949P.
XX 12-MAR-1999; 99US-0123951P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136437P.
XX 28-MAY-1999; 99US-0136439P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 28-MAY-1999; 99US-0137567P.
XX 29-JUN-1999; 99US-0141448P.
XX 27-AUG-1999; 99US-0151114P.
XX 03-SEP-1999; 99US-0152524P.
XX 29-SEP-1999; 99US-0156555P.
XX 29-SEP-1999; 99US-0156633P.
XX 29-SEP-1999; 99US-0156634P.
XX 29-SEP-1999; 99US-0156653P.
XX 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.
 PR 01-OCT-1999; 99US-0157283P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 PR 12-OCT-1999; 99US-00417044.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
 XX
 DR WPI; 2000-317986/27.
 DR N-PSDB; AAA46116.
 XX
 PT Non-endogenous, human G protein-coupled receptors for screening receptor,
 PT inverse or partial agonists useful as therapeutic agents.
 XX
 PS Example 2; Page 168-169; 187pp; English.
 XX
 CC The present invention describes transmembrane receptors, preferably human
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is
 CC unknown (orphan GPCR receptors). More specifically the present invention
 CC relates to non-endogenous, constitutively activated versions of a human
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct
 CC identification of candidate compounds as receptor agonists, inverse
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 412 AA;
 Query Match 99.7%; Score 2149; DB 3; Length 412;
 Best Local Similarity 99.8%; Pred. No. 1.4e-194;
 Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFFLGALVPVTAVALCLFVVGSGNVTV 60
 Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFFLGALVPVTAVALCLFVVGSGNVTV 60
 QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLCLSLIYVGE 120
 Db 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLCLSLIYVGE 120
 QY 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVIAVALLSAGPFLFLVGVE 180
 Db 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVIAVALLSAGPFLFLVGVE 180
 QY 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAAALFSRECRPSPA 240
 Db 181 QDPGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAAALFSRECRPSPA 240
 QY 241 QLGALRVMLVMTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRERGHQTIVRL 300
 Db 241 QLGALRVMLVMTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRERGHQTIVRL 300
 QY 301 LVVLAFTICMLPFHVGRIIYINTEDSRMTYFQVFNIVALQLFYLASINPILYNLISK 360
 Db 301 LVVLAFTICMLPFHVGRIIYINTEDSRMTYFQVFNIVALQLFYLASINPILYNLISK 360
 QY 361 KYRAAFAKLLARKRPRGHRSDTAGEVAGDTGGDTVGYTETSANVKTNG 412
 Db 361 KYRAAFAKLLARKRPRGHRSDTAGEVAGDTGGDTVGYTETSANVKTNG 412
 RESULT 11
 ADG86491
 ID ADG86491 standard; protein; 412 AA.
 XX
 AC ADG86491;
 XX
 DT 11-MAR-2004 (first entry)
 XX

DE Human hGPR38 V297K mutant protein.
 XX
 KW Human; receptor; mutein; endogenous orphan GPCR;
 KW G protein-coupled receptor; transmembrane domain 6; mutant.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US2003229216-A1.
 XX
 PD 11-DEC-2003.
 XX
 PF 16-APR-2003; 2003US-00417820.
 XX
 PR 13-OCT-1998; 98US-00170496.
 PR 12-NOV-1998; 98US-0108029P.
 PR 20-NOV-1998; 98US-0109213P.
 PR 27-NOV-1998; 98US-0110060P.
 PR 16-FEB-1999; 99US-0120416P.
 PR 26-FEB-1999; 99US-0121852P.
 PR 12-MAR-1999; 99US-0123944P.
 PR 12-MAR-1999; 99US-0123945P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 12-MAR-1999; 99US-0123948P.
 PR 12-MAR-1999; 99US-0123949P.
 PR 12-MAR-1999; 99US-0123951P.
 PR 28-MAY-1999; 99US-0136436P.
 PR 28-MAY-1999; 99US-0136437P.
 PR 28-MAY-1999; 99US-0136439P.
 PR 28-MAY-1999; 99US-0136567P.
 PR 28-MAY-1999; 99US-0137127P.
 PR 28-MAY-1999; 99US-0137131P.
 PR 29-JUN-1999; 99US-041448P.
 PR 27-AUG-1999; 99US-0151114P.
 PR 03-SEP-1999; 99US-0152524P.
 PR 29-SEP-1999; 99US-0156555P.
 PR 29-SEP-1999; 99US-0156633P.
 PR 29-SEP-1999; 99US-0156634P.
 PR 29-SEP-1999; 99US-0156653P.
 PR 01-OCT-1999; 99US-0157280P.
 PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.
 PR 01-OCT-1999; 99US-0157293P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 XX
 PA (CHEN/) CHEN R.
 PA (LIAW/) LIAW C W.
 PA (LOWI/) LOWITZ K.
 PA (CHAL/) CHALMERS D T.
 PA (BEHA/) BEHAN D P.
 XX
 PI Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;
 XX
 DR WPI; 2004-052038/05.
 DR N-PSDB; ADG86490.
 XX
 PT New cDNA encoding a non-endogenous, constitutively activated version of a
 PT human G protein-coupled receptor, useful for identifying receptor,
 PT inverse or partial agonists having potential applicability as therapeutic
 PT agents.
 XX
 PS Example 2; SEQ ID NO 130; 110pp; English.
 XX
 CC The invention relates to a cDNA encoding a non-endogenous, constitutively
 CC activated version of a human G protein-coupled receptor comprising HARE-
 CC 3(F313K), HARE-4(V233K), HARE-5(A240K), HGPCR14(L257K), HGPCR27(C283K),
 CC HARE-1(E232K), HARE-2(G285K), hRUP1(L239K), hG2A(K232A), hRUP3(L224K),
 CC hRUP5(A236K), hRUP6(N267K), hRUP7(A302K), hCHN4(V236K), hMC4(V244K),
 CC hCHN3(S284K), hCHN6(L352K), hCHN8(N235K) or hH9(F236K). Also included are
 CC a non-endogenous version of a human G protein-coupled receptor encoded by
 CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell
 CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively

CC activated version of a human G protein-coupled AT1 receptor comprising
CC the angiotensin II type 1 receptor hAT1(F239K), hAT1(N111A),
CC hAT1(AT2K255IC3, a domain swap mutant) or hAT1(A243+). The mutation is of
CC an amino acid 16 residues from the proline in transmembrane domain 6 and
CC is usually to a lysine. The cDNA is useful for identifying candidate
CC compounds as receptor agonists, inverse agonists or partial agonists
CC having potential applicability as therapeutic agents. The present
CC sequence represents a mutated human GPCR.
XX
SQ Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 8; Length 412;
Best Local Similarity 99.8%; Pred. No. 1.4e-194;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MGSPWNGSDGEGAREPPWALPPCDERRCPFFLGALVPVTA VCLCLFVVGSGNVTV 60
Db 1 MGSPWNGSDGEGAREPPWALPPCDERRCPFFLGALVPVTA VCLCLFVVGSGNVTV 60
Qy 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120
Db 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120
Qy 121 CTYATLLHMTALSVRYLAICPLRVLVTRRVRALIAVLAVALLSAGPFLVGV 180
Db 121 CTYATLLHMTALSVRYLAICPLRVLVTRRVRALIAVLAVALLSAGPFLVGV 180
Qy 181 QDPGISVVGNGTARIASSPLASSPPLWLRAPPSPSPETAEEAALFSRECRPSPA 240
Db 181 QDPGISVVGNGTARIASSPLASSPPLWLRAPPSPSPETAEEAALFSRECRPSPA 240
Qy 241 QLGALRVMLVWTVAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTKRVL 300
Db 241 QLGALRVMLVWTVAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTKRVL 300
Qy 301 LVVVLAFIICWLPFHVGRHIIINTEDSRMYPFSQYFNIVALQLFYLSASINPILYNLSK 360
Db 301 LVVVLAFIICWLPFHVGRHIIINTEDSRMYPFSQYFNIVALQLFYLSASINPILYNLSK 360
Qy 361 KYRAAFKLLARKSRPGRFHSRDTAGEVAGDTGGDTGVGTSTANVKTWG 412
Db 361 KYRAAFKLLARKSRPGRFHSRDTAGEVAGDTGGDTGVGTSTANVKTWG 412

RESULT 12
ADG86511
ID ADG86511 standard; protein; 412 AA.
XX ADG86511;
AC ADG86511;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human orphan GPCR-associated protein #2.
XX
KW Human; endogenous orphan GPCR; G protein-coupled receptor;
KW transmembrane domain 6.
XX
OS Homo sapiens.
XX
FN US2003229216-A1.
XX
PD 11-DEC-2003.
XX
PF 16-APR-2003; 2003US-00417820.
XX
PR 13-OCT-1998; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123945P.

PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-0141448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
XX
(CHEN/) CHEN R.
PA (LIAW/) LIAW C W.
PA (LOWI/) LOWITZ K.
PA (CHAL/) CHALMERS D T.
XX (BEHA/) BEHAN D P.

PI Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;
XX WPI; 2004-052038/05.
XX
PT New cDNA encoding a non-endogenous, constitutively activated version of a
PT human G protein-coupled receptor, useful for identifying receptor,
PT inverse or partial agonists having potential applicability as therapeutic
PT agents.

Discloure; SEQ ID NO 150; 110pp; English.

CC The invention relates to a cDNA encoding a non-endogenous, constitutively
CC activated version of a human G protein-coupled receptor comprising HARE-
CC 3(F313K), HARE-4(V233K), HARE-5(A240K), HGPCR14(L257K), HGPCR27(C283K),
CC HARE-1(E232K), HARE-2(G285K), hPRP1 (L239K), hG2A(K232A), hRUP3(L224K),
CC hRUP5(A236K), hRUP6(N267K), hRUP7(A302K), hCHN4(V236K), hMC4(V244K),
CC hCHN3(S284K), hCHN6(L352K), hCHN8(N235K) or hH9(F236K). Also included are
CC a non-endogenous version of a human G protein-coupled receptor encoded by
CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell
CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively
CC activated version of a human G protein-coupled AT1 receptor comprising
CC the angiotensin II type 1 receptor hAT1(F239K), hAT1(N111A),
CC hAT1(AT2K255IC3, a domain swap mutant) or hAT1(A243+). The mutation is of
CC an amino acid 16 residues from the proline in transmembrane domain 6 and
CC is usually to a lysine. The cDNA is useful for identifying candidate
CC compounds as receptor agonists, inverse agonists or partial agonists
CC having potential applicability as therapeutic agents. The present
CC sequence is a GPCR-associated protein included in the sequence listing
CC but not mentioned anywhere else in the specification.

SQ Sequence 412 AA;

Query Match 99.7%; Score 2149; DB 8; Length 412;
Best Local Similarity 99.8%; Pred. No. 1.4e-194;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MGSPWNGSDGEGAREPPWALPPCDERRCPFFLGALVPVTA VCLCLFVVGSGNVTV 60
Db 1 MGSPWNGSDGEGAREPPWALPPCDERRCPFFLGALVPVTA VCLCLFVVGSGNVTV 60
Qy 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120
Db 61 MLIGRYDMRTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPVFGPLLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVRYLAICRPLRAVLTERRVRLIAVLWAVALLSAGPFLVLGVGE 180
Db 121 CTYATLLHMTALSVRYLAICRPLRAVLTERRVRLIAVLWAVALLSAGPFLVLGVGE 180
QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
Db 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
QY 241 QLGALRVMLWVTYAFYLPFLCLSLYGLIGRELWSSRRPLRGAASGRGRHQTQVRL 300
Db 241 QLGALRVMLWVTYAFYLPFLCLSLYGLIGRELWSSRRPLRGAASGRGRHQTQVRL 300
QY 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLSASINPILYNLISK 360
Db 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLSASINPILYNLISK 360
QY 361 KYRAAFKLLIARKSRPRGHRSDTAGEVAGDTGDTGVGYTETSANVKTMG 412
Db 361 KYRAAFKLLIARKSRPRGHRSDTAGEVAGDTGDTGVGYTETSANVKTMG 412

RESULT 13
ADP20284
ID ADP20284 standard; protein; 412 AA.
XX AC ADP20284;
XX DT 26-AUG-2004 (first entry)
XX DE Human GPCR GPR38 V297K mutant.
XX KW antiinflammatory; GPCR-agonist; GPCR-antagonist;
KW G protein-coupled receptor; GPCR; GPCR modulator; inflammation;
KW pharmaceutical composition; inflammatory disorder; human; hGPR38; mutant;
mutin.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2004110238-A1.
XX PD 10-JUN-2004.
XX PF 26-NOV-2003; 2003US-00723955.
XX PR 13-OCT-1998; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-0144489P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 01-OCT-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.

PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 16-APR-2003; 2003US-00417820.
XX (CHEN/) CHEN R.
PA (LIAM/) LIAM C W.
PA (LOWI/) LOWITZ K.
PA (CHAL/) CHALMERS D T.
XX (BEHA/) BEHAN D P.
PI Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;
XX WPI; 2004-440359/41.
DR N-PSDB; ADP20283.
XX
PT Identifying one or more candidate compounds as a modulator of a G protein
PT coupled receptor (GPCR), useful for treating disorders or conditions
PT associated with expression or activity of the GPCR.
XX
PS Example 2; SEQ ID NO 130; 106pp; English.
XX
CC The invention describes a method of identifying one or more candidate
CC compounds as a modulator of a G protein-coupled receptor that comprises a
CC fully defined sequence of 337 amino acids (SEQ ID NO: 82), comprising
CC contacting the one or more compounds with a host cell or with a membrane
CC of a host cell that expresses the receptor, and measuring the ability of
CC the compound or compounds to inhibit or stimulate functionality of the
CC receptor. Also described are: a method for identifying one or more
CC candidate compounds as a modulator of inflammation; a method for
CC identifying one or more candidate compounds as a modulator of a G protein
CC coupled receptor; a compound identified by any of the methods cited
CC above; a pharmaceutical composition; a method of modulating the activity
CC of a G protein-coupled receptor having the amino acid sequence of SEQ ID
CC NO:82; a method of modulating inflammation in a mammal in need of the
CC modulating; a method of inhibiting inflammation in a mammal in need of
CC the inhibiting; a method of preventing or treating an inflammatory
CC disorder in a mammal in need of the preventing or treating; and a method
CC of treating an inflammatory disorder. The methods and compositions of the
CC present invention are useful for the treatment of diseases or conditions
CC associated with aberrant expression or activity of the GPCR e.g.
CC inflammation. This is the amino acid sequence of human G protein coupled
CC receptor (GPCR) hGPR38 V297K mutant.
XX
SQ Sequence 412 AA;
Query Match 99.7%; Score 2149; DB 8; Length 412;
Best Local Similarity 99.8%; Pred. No. 1.4e-194;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPEGAREPPHPALPPCDERRCSPPFICALVPVTVAVCLCLFVGVGNGVTV 60
Db 1 MGSPWNGSDGPEGAREPPHPALPPCDERRCSPPFICALVPVTVAVCLCLFVGVGNGVTV 60
QY 61 MLIGRYRDMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPWFGPCLCLSLYVGBG 120
Db 61 MLIGRYRDMRTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPWFGPCLCLSLYVGBG 120
QY 121 CTYATLLHMTALSVRYLAICRPLRAVLTERRVRLIAVLWAVALLSAGPFLVLGVGE 180
Db 121 CTYATLLHMTALSVRYLAICRPLRAVLTERRVRLIAVLWAVALLSAGPFLVLGVGE 180
QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
Db 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
QY 241 QLGALRVMLWVTYAFYLPFLCLSLYGLIGRELWSSRRPLRGAASGRGRHQTQVRL 300
Db 241 QLGALRVMLWVTYAFYLPFLCLSLYGLIGRELWSSRRPLRGAASGRGRHQTQVRL 300
QY 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLSASINPILYNLISK 360
Db 301 LVVVLAFIICWLPFHVGRIIYINTEDSRMVFSQYFNIVALQLFYLSASINPILYNLISK 360

Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLASINPILYNLISK 360
 QY 361 KYRAAFKLLARKSRPRGHRSDTAGEVAGDTGGDTGVGTETSANVKTWG 412
 Db 361 KYRAAFKLLARKSRPRGHRSDTAGEVAGDTGGDTGVGTETSANVKTWG 412

RESULT 14

ABB09535
 ID ABB09535 standard; protein; 412 AA.

XX ABB09535;

XX 22-OCT-2002 (first entry)

XX Human motilin receptor.

XX Human; motilin receptor; appetite; food intake; agonist; analogue;
 KW undernutrition; anorexia; cachexia; malignant disease; infection;
 KW inflammatory disease; weight loss; antagonist; obesity; anorectic;
 KW anabolic; ghrelin receptor homologue; receptor.

XX Homo sapiens.

XX WO200260472-A1.

XX 08-AUG-2002.

XX 31-JAN-2002; 2002WO-JP000765.

XX 31-JAN-2001; 2001JP-00024423.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Inui A, Asakawa A, Kaga T;

XX WPI; 2002-619206/66.

XX Remedies for diseases with hypo-nutrition status e.g. inappetence and
 PT cachexia, containing ghrelin or its analogs including agonists and
 PT antagonists.

XX Disclosure; Fig 1B; 50pp; Japanese.

XX The invention relates to the use of ghrelin or its analogues for the
 CC treatment of diseases associated with undernutrition such as anorexia,
 CC and also relates to the use of ghrelin antagonists for the prevention or
 CC treatment of obesity. The invention additionally discloses a method for
 CC screening ghrelin agonists or antagonists by measuring the amount of food
 CC intake, neuropeptide Y (NPY) expression, binding of NPY to NPY receptor
 CC Y1, oxygen consumption, gastric emptying, or activity of the vagus nerve.
 CC Intracerebroventricular (ICV) administration of ghrelin in animals was
 CC found to increase food intake over a period of 24 hours. Ghrelin and its
 CC analogues may therefore be used to treat conditions such as loss of
 CC appetite, anorexia, cachexia, malignant diseases, and weight loss
 CC associated with infection or inflammatory diseases. Conversely, ghrelin
 CC antagonists may be used in the treatment of obesity. The present sequence
 CC represents the human motilin receptor, a homologue of the ghrelin
 CC receptor (ABB09534) which is referred to in the disclosure of the
 CC invention

XX Sequence 412 AA;

Query Match 99.4%; Score 2141; DB 5; Length 412;

Best Local Similarity 99.5%; Pred. No. 8e-194; Mismatches 0; Gaps 0;
 Matches 410; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAREPPWLPALPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60

Db 1 MGSPWNGSDGPGAREPPWLPALPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60

QY 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120

|||||

Db 61 MLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120
 QY 121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE 180
 Db 121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE 180
 QY 181 QDPGISVVPGLNGTARTIASSPLASPPPLWLSRAPPPSPGPETAAALFSRECRPSA 240
 Db 181 QDPGISVVPGLNGTARTIASSPLASPPPLWLSRAPPPSPGPETAAALFSRECRPSA 240
 QY 241 QLGALRYMLWVTTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGRHROTIVRL 300
 Db 241 QLGALRYMLWVTTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGRHROTIVRL 300
 QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLASINPILYNLISK 360
 Db 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFYQYFNIVALQLFYLASINPILYNLISK 360
 QY 361 KYRAAFKLLARKSRPRGHRSDTAGEVAGDTGGDTGVGTETSANVKTWG 412
 Db 361 KYRAAFKLLARKSRPRGHRSDTAGEVAGDTGGDTGVGTETSANVKTWG 412

RESULT 15

ADN12079

ID ADN12079 standard; protein; 412 AA.

XX AC ADN12079;

XX 17-JUN-2004 (first entry)

XX Protein #4 associated with growth hormone secretagogue receptor.

XX diabetes; growth hormone secretagogue receptor; GHS-R; Antidiabetic;

XX Anorectic; obesity; blood sugar level; appetite.

XX Homo sapiens.

XX WO2004004772-A1.

XX 15-JAN-2004.

XX 03-JUL-2003; 2003WO-JP008482.

XX 05-JUL-2002; 2002JP-00197582.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Inui A, Asakawa A;

XX WPI; 2004-099347/10.

XX Growth hormone secretagogue receptor antagonist for treatment of
 PT diabetes, obesity and appetite control.

XX Disclosure; SEQ ID NO 4; 44pp; Japanese.

XX The present invention relates to a treatment and preventative agent for
 CC diabetes comprises growth hormone secretagogue receptor (GHS-R)
 CC antagonist. For treatment and prevention of diabetes, obesity, for
 CC lowering blood sugar levels and for use in controlling appetite. The
 CC present sequence represents a protein associated with growth hormone
 CC secretagogue receptor.

XX Sequence 412 AA;

Query Match 99.4%; Score 2141; DB 8; Length 412;

Best Local Similarity 99.5%; Pred. No. 8e-194;
 Matches 410; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAREPPWLPALPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60

Db 1 MGSPWNGSDGPGAREPPWLPALPCDERRCSPFPLGALVPVTVAVCLCLFVVGSGNVTV 60

Qy	61	MLIGRYEDMETTNLYLGSMAVSDLLILLGLPFOLYRLWRSRPWVFGPILLCRLSLYVGE	120
Db	61	MLIGRYEDMETTNLYLGSMAVSDLLILLGLPFOLYRLWRSRPWVFGPILLCRLSLYVGE	120
Qy	121	CTYATLLHMTALSVERYLAICRPLRARLVTRRRVRALIAVLWAVALLSAGPFLVGV	180
Db	121	CTYATLLHMTALSVERYLAICRPLRARLVTRRRVRALIAVLWAVALLSAGPFLVGV	180
Qy	181	QDFGISVVPGLNGTARIASSPLASSPPLMLSRAPPPSPGPETAEEAALFSRECRPSA	240
Db	181	QDFGISVVPGLNGTARIASSPLASSPPLMLSRAPPPSPGPETAEEAALFSRECRPSA	240
Qy	241	QLGALRVMLWVTTAYFFLPFLCLSIYGLIGRELWSSRRPLRGPAASGRGHRQTVRL	300
Db	241	QLGALRVMLWVTTAYFFLPFLCLSIYGLIGRELWSSRRPLRGPAASGRGHRQTVRL	300
Qy	301	LVVVLAFFIICWLPFHVGRIIYINTEDSRMMYFSQYENIVALQLFYLSASINPILYNLISK	360
Db	301	LVVVLAFFIICWLPFHVGRIIYINTEDSRMMYFSQYENIVALQLFYLSASINPILYNLISK	360
Qy	361	KYRAAAFKLLARSRGRGHRSDTAGEVAGDTGGDTVGYTETSANVKTMG	412
Db	361	KYRAAAFKLLARSRGRGHRSDTAGEVAGDTGGDTVGYTETSANVKTMG	412

Search completed: April 11, 2005, 21:02:39
Job time : 72.6667 secs

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OM protein - protein search, using sw model

Run on: April 11, 2005, 20:05:13 ; Search time 21.1679 Seconds
(without alignments)
1452.926 Million cell updates/sec

Title: US-09-719-485-3

Perfect score: 2155

Sequence: 1 MGSPWNGSDGEGAREPPWP.....DTGDDTVGYTETSANVKMG 412

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

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6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2155	100.0	412	US-09-743-742B-8	Sequence 8, Appli
2	865.5	40.2	349	US-09-762-661A-2	Sequence 2, Appli
3	864.5	40.1	366	US-09-762-661A-7	Sequence 7, Appli
4	864.5	40.1	366	US-09-743-475-6	Sequence 6, Appli
5	863.5	40.1	366	US-09-077-675A-13	Sequence 13, Appli
6	863.5	40.1	366	US-09-077-674-13	Sequence 13, Appli
7	863.5	40.1	366	US-09-170-496D-88	Sequence 8, Appli
8	863.5	40.1	366	US-09-743-742B-7	Sequence 7, Appli
9	863.5	40.1	366	US-09-762-661A-5	Sequence 5, Appli
10	863.5	40.1	366	US-09-364-425B-45	Sequence 45, Appli
11	863.5	40.1	366	US-09-743-475-4	Sequence 4, Appli
12	863	40.0	353	US-09-077-675A-3	Sequence 3, Appli
13	863	40.0	353	US-09-077-674-3	Sequence 3, Appli
14	861.5	40.0	364	US-09-077-675A-16	Sequence 16, Appli
15	861.5	40.0	364	US-09-077-674-16	Sequence 16, Appli
16	861.5	40.0	364	US-09-762-661A-6	Sequence 6, Appli
17	861.5	40.0	364	US-09-743-475-3	Sequence 3, Appli
18	861.5	40.0	364	US-09-743-475-5	Sequence 5, Appli
19	860	39.9	361	US-09-077-675A-8	Sequence 8, Appli
20	860	39.9	361	US-09-077-674-8	Sequence 8, Appli
21	857.5	39.8	366	US-09-170-496D-210	Sequence 210, App
22	775.5	36.0	302	US-09-077-675A-2	Sequence 2, Appli
23	775.5	36.0	302	US-09-077-674-2	Sequence 2, Appli
24	774.5	35.9	302	US-09-077-675A-7	Sequence 7, Appli
25	774.5	35.9	302	US-09-077-674-7	Sequence 7, Appli
26	674.5	31.3	271	US-09-077-675A-12	Sequence 12, Appli
27	674.5	31.3	271	US-09-077-674-12	Sequence 12, Appli

28	644.5	29.9	289	3	US-09-077-675A-10	Sequence 10, Appli
29	644.5	29.9	289	4	US-09-077-674-10	Sequence 10, Appli
30	633	29.4	289	3	US-09-077-675A-5	Sequence 5, Appli
31	633	29.4	289	4	US-09-077-674-5	Sequence 5, Appli
32	497	23.1	418	4	US-09-743-742B-5	Sequence 5, Appli
33	491	22.8	418	4	US-09-826-509-535	Sequence 535, App
34	485.5	22.5	403	4	US-09-170-496D-114	Sequence 114, App
35	485.5	22.5	403	4	US-09-743-742B-4	Sequence 4, Appli
36	485.5	22.5	403	4	US-09-743-742B-10	Sequence 10, Appli
37	483.5	22.4	403	4	US-09-170-496D-224	Sequence 224, App
38	483	22.4	415	4	US-09-341-016A-1	Sequence 1, Appli
39	479	22.2	415	4	US-09-545-944-2	Sequence 2, Appli
40	476	22.1	412	4	US-09-949-016-10101	Sequence 10101, A
41	466	21.6	353	1	US-08-118-270-45	Sequence 45, Appli
42	466	21.6	353	5	PCT-US93-08528-45	Sequence 45, Appli
43	457.5	21.2	405	4	US-09-743-742B-2	Sequence 2, Appli
44	457.5	21.2	405	4	US-09-743-742B-11	Sequence 11, Appli
45	413	19.2	410	3	US-08-858-876A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-743-742B-8

; Sequence 8, Application US/09743742B

; Patent No. 6599718

; GENERAL INFORMATION:

; APPLICANT: Liu, Qingyun

; APPLICANT: Howard, Andrew D.

; APPLICANT: McKee, Karen Kulju

; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED

; TITLE OF INVENTION: RECEPTORS AND NUCLEIC ACIDS

; FILE REFERENCE: 20217YP

; CURRENT APPLICATION NUMBER: US/09/743,742B

; PRIORITY FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: PCT/US99/15941

; PRIOR FILING DATE: 1999-07-13

; PRIOR APPLICATION NUMBER: 60/092,623

; PRIOR FILING DATE: 1998-07-13

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 412

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-743-742B-8

Query Match 100.0%; Score 2155; DB 4; Length 412;

Best Local Similarity 100.0%; Pred. No. 3,7e-177;

Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSPWNGSDGEGAREPPWPALPPCDERRCPPELPGALVPVTAVCLCLFVVGVSGNVTV	60
Db	1	MGSPWNGSDGEGAREPPWPALPPCDERRCPPELPGALVPVTAVCLCLFVVGVSGNVTV	60
Qy	61	MLIGRYDMRTTNYLGSMAVSDLLILGLPFDLYRLWRSRPMWFGPFLCLSLYVGE	120
Db	61	MLIGRYDMRTTNYLGSMAVSDLLILGLPFDLYRLWRSRPMWFGPFLCLSLYVGE	120
Qy	121	CTYATLHMTALSVERVLAICRPLRARVLVTRRRVRAIIVLWVALLSAGPFLVGV	180
Db	121	CTYATLHMTALSVERVLAICRPLRARVLVTRRRVRAIIVLWVALLSAGPFLVGV	180
Qy	181	ODRGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPETAALFSSRCRPSPA	240
Db	181	ODRGISVVGGLNGTARIASSPLASSPPLWLSRAPPPSPETAALFSSRCRPSPA	240
Qy	241	QLGARVLMVWTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQT	300
Db	241	QLGARVLMVWTYATFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQT	300
Qy	301	LVVVLAFTICWLPHVGRRIIYINTEDSRMMYFSQYFNIVALQLFVLSASINPILY	360
Db	301	LVVVLAFTICWLPHVGRRIIYINTEDSRMMYFSQYFNIVALQLFVLSASINPILY	360

Db 301 LVVLAFLICWLPFHVGRYYINTEDSRMMYFSQYFNIVALQLFYLASINPILYNLSK 360
QY 361 KYRAAFKLLARKSPRGFHSRDTAGEVAGDTGDTVGYTETSANVKTMG 412
Db 361 KYRAAFKLLARKSPRGFHSRDTAGEVAGDTGDTVGYTETSANVKTMG 412

RESULT 2

US-09-762-661A-2
; Sequence 2, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Palyha, Oksana C.
; APPLICANT: Smith, Roy G.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-762-661A-2

Query Match 40.2%; Score 865.5; DB 4; Length 349;
Best Local Similarity 46.4%; Pred. No. 1.8e-66;
Matches 187; Conservative 50; Mismatches 97; Indels 69; Gaps 8;

QY 14 AREPP-----WPALPPCDERRCPFFLGALVPVTAIVCLCFVVGSGNVVTVMLIGRYDM 69
Db 6 AREGSGAGWDLIP-----LFAPLAGVTATCVAFVGVAGNLLTVLIVRRFREL 57
QY 70 RTTNLYLGSMAVSDLLILGLPFDLYLWRSRPVWFGELLCRLSLYVGEQCTYATLLHM 129
Db 58 RTTNLYLCSLACSLLILFLCPLDLVRLWQYRPWTFGLDKLQFVSEGCYATVLT 117
QY 130 TALSVERYLAI CRPIRARVLVTRRRVRLIALVMAVALLSAGPFLVGVGEQDPGISVVP 189
Db 118 TALSVERYPACFPURAKVLVTKGRVKLALLAIWAFVAFCSAGPITVLVGEHE----- 170
QY 190 GUNGRTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPS--PAQLGALRV 247
Db 171 --NGT-----DPRD-----TRECRATEFAVRGSLITA 195
QY 248 MLWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASRGHGRQTVRLVLLVVVLAP 307
Db 196 MYWSSVFFFLPVFCLTVLYGLIGRLWRRGRGDTAGGASLREQSHRQTVKMLAVVWVAF 255
QY 308 IICWLPFHVGRYYINTEDS---RMMYFSQYFNIVALQLFYLASINPILYNLSKYYRA 364
Db 256 IFCWLPFHVGRYLFKSFGSLEIAQISOYCNLVSVFLFYLSAINPILYNIMSKYRV 315
QY 365 AAFKLLARKSPRGFHSRDTAGEVAGDTGDTVGYTETSAN 407
Db 316 AVFKLLGFPFPQSKLSTLKDESSR-----AWTESSIN 348

RESULT 3

US-09-762-661A-7
; Sequence 7, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.

; APPLICANT: Palyha, Oksana C.
; APPLICANT: Smith, Roy G.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-762-661A-7

Query Match 40.1%; Score 864.5; DB 4; Length 366;
Best Local Similarity 45.1%; Pred. No. 2.3e-66;
Matches 189; Conservative 55; Mismatches 104; Indels 71; Gaps 10;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTAIVCLCFVVGSGN 56
Db 2 WNATPSEPGPNLTLPDLGWDAPPENDSLVEELLPLFPPTPLAGVTATCVAFVVGIAGN 61
QY 57 VVTWMLIGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLWRSRPVWFGELLCRLSLY 116
Db 62 LITMLVWSRFREMTTNLYLSSMAFSDLLIFLCMPDLDFRLWQYRPMNLGNLCKLPQF 121
QY 117 VGEQCTYATLLHMTALSVERYLAI CRPIRARVLVTRRRVRLIALVMAVALLSAGPFLFL 176
Db 122 VSECTTATVLTITALSVERYPALCFPLRAKVWTKGRVKVLIVMAVAFCSAGPFLV 181
QY 177 VGVQDPGISVVGUNGRTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
Db 182 VGVHEH-----NGT-----DPRD-----TNECR 199
QY 237 PS--PAQLGALRVMLWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASG---RER 291
Db 200 ATEFAVRSGLLTVWVWSSVFFFLVFLVCLTVLYSLIGRKLW---RRKRGEAAVGSRLDQ 256
QY 292 GHROTIVRLVVLAFIICWLPFHVGRYY---INTEDSRMMYFSQYFNIVALQLFYL 348
Db 257 NIKOTVRLVAVVFAFVLCWLPFHVGRYLFKSLEPGSVEIAQISOYCNLVSVFLFYLSA 316
QY 349 SINPILYNLSKYYRAAFKLLARKSPRGFHSRDTAGEVAGDTGDTVGYTETSAN 407
Db 317 AINPILYNIMSKYRVAVFKLLGFPFPQSKLSTLKDESSR-----AWTESSIN 365

RESULT 4

US-09-743-475-6
; Sequence 6, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10

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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-743-475-6

Query Match      40.1%; Score 864.5; DB 4; Length 366;
Best Local Similarity 45.1%; Pred. No. 2.3e-66;
Matches 189; Conservative 55; Mismatches 104; Indels 71; Gaps 10;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTAVALCLFVVGSGN 56
DB 2 WNA TPSEEPGNLTLPDLGWDAPPENDSLVBELLPLFTPLLAGVTATCATVALFVVGIA 61

QY 57 VVTVMILGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWFGPLLCRLSLY 116
DB 62 LTLMLVSRFRMRTTNNLYLSSMAFSDLLIFLCMLDPLDLFRWQYRPNLGNLLCKLFQF 121

QY 117 VGECTYATLHMTALSVERYLAI CRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFL 176
DB 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTYKGRVILVIMAVAFCSAGPIFVL 181

QY 177 VGVQDPCGISVVGINGLTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
DB 182 VGVHEH-----NGT-----DPRD-----TNECR 199

QY 237 PS--PAQIGALRVMLVTTAYFFLPFLCLSLYGLIGRELSSRPLRGPAASG---RER 291
DB 200 ATEFAVRSGLLTVMVWVSFFFLFVFCFLTVLSYLGRLKLM---RRKGEAAVGSRLDQ 256

QY 292 GHQTVRVLLVVLAFIICWLPFHVGRIIY---INTEDSRMYFSQYFNIVALQLFYLSA 348
DB 257 NHQTVKMLAVVFAFICWLPFHVGRIYLFPSKLEPGSVETAIQISQYCNLVSVFLYLSA 316

QY 349 SINPLYNLISKYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVGYTETSAN 407
DB 317 AINPLYNIMSKYRAVAVFKLIGLGFPPFQKLSLTKDESSR-----AWTESSIN 365

RESULT 5
US-09-077-675A-13
; Sequence 13, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-675A-13

Query Match      40.1%; Score 863.5; DB 3; Length 366;
Best Local Similarity 44.7%; Pred. No. 2.9e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTAVALCLFVVGSGN 56
DB 2 WNA TPSEEPGNLTADLDWDASFGNDSLGDELLQLFPAPLLAGVTATCATVALFVVGIA 61

QY 57 VVTVMILGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWFGPLLCRLSLY 116
DB 62 LTLMLVSRFRMRTTNNLYLSSMAFSDLLIFLCMLDPLDLVRLWQYRPNWFGDLCKLFQF 121

QY 117 VGECTYATLHMTALSVERYLAI CRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFL 176
DB 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTYKGRVILVIMAVAFCSAGPIFVL 181

QY 177 VGVQDPCGISVVGINGLTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
DB 182 VGVHEH-----NGT-----DP--W-----DTNECR 199

QY 237 PS--PAQIGALRVMLVTTAYFFLPFLCLSLYGLIGRELSSRPLRGPAASGRGHR 294
DB 200 PTEFAVRSGLLTVMVWVSIFFLFVFCFLTVLSYLGRLKLMRRRRRGDAVVGASLRDQNHK 259

QY 295 QTVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
DB 260 QTVKMLAVVFAFICWLPFHVGRIYLFPSKLEPGSVETAIQISQYCNLVSVFLYLSA 319

QY 352 PILYNLISKYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVGYTETSAN 407
DB 320 PILYNIMSKYRAVAVFKLIGLGFPPFQKLSLTKDESSR-----AWTESSIN 365

RESULT 6
US-09-077-674-13
; Sequence 13, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/077,674
/ FILING DATE: 3-JUN-1998
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cocuzzo, Anna L.
/ REGISTRATION NUMBER: 42,452
/ REFERENCE/DOCKET NUMBER: 19589P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 732-594-1273
/ TELEFAX: 732-594-4720
/
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 366 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-09-077-674-13

Query Match          40.1%; Score 863.5; DB 4; Length 366;
Best Local Similarity 44.7%; Pred. No. 2.9e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTAVALCLFVVGSGN 56
Db 2 WNATPSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVAFVVGIA 61
QY 57 VVTWMLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWFGPLLCRLSLY 116
Db 62 LITLWLVSRFRELRTTNNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPMNFGDLLCKLQF 121
QY 117 VGEGETATLLHMTALSVRYLAICRPLRARVLTNRVRLALIAVLWAVALLSAGPFLFL 176
Db 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFWIAVAFCSAGPIFVL 181
QY 177 VGEQDPGISVVGINGTARIASSPLASSPPLWLSRAPPPSPGPETAFAAALFSRBCR 236
Db 182 VGVHE-----NGT-----DP-W-----DTNECR 199
QY 237 PS--PAQLGALRWLVTTAYFFLPCLLSILYGLIGBELWSSRRPLRGPAASGRGHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259
QY 295 QTVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
Db 260 QTVKMLAVVVFAPILCWLPFHVGRLYFSKSPGPSLEIAQISQYCNLVSVFLFYLSAIN 319
QY 352 PILYNLSKYYRAAFKLLARKSRPRGHRSDTAGVAGDTGGDTVGYTETSAN 407
Db 320 PILYNIMSKYRVAVFRLGPEFQSQRKSLTKDESSR-----AWTESSIN 365

RESULT 8
US-09-743-742B-7
/ Sequence 7, Application US/09743742B
/ Patent No. 6559718
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Qingyun
/ APPLICANT: Howard, Andrew D.
/ APPLICANT: McKee, Karen Kulju
/ TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED
/ FILE OF INVENTION: RECEPTORS AND NUCLEIC ACIDS
/ FILE REFERENCE: 20217P
/ CURRENT APPLICATION NUMBER: US/09/743,742B
/ PRIOR FILING DATE: 2001-03-15
/ PRIOR APPLICATION NUMBER: PCT/US99/15941
/ PRIOR FILING DATE: 1999-07-13
/ PRIOR APPLICATION NUMBER: 60/092,623
/ PRIOR FILING DATE: 1998-07-13
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 7
/ LENGTH: 366
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/
US-09-743-742B-7

Query Match          40.1%; Score 863.5; DB 4; Length 366;
Best Local Similarity 44.7%; Pred. No. 2.9e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWPALPPCD---ERRCSPFPLGALVPVTAVALCLFVVGSGN 56
Db 2 WNATPSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVAFVVGIA 61
QY 57 VVTWMLIGRYDMRTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWFGPLLCRLSLY 116
Db 62 LITLWLVSRFRELRTTNNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPMNFGDLLCKLQF 121
QY 117 VGEGETATLLHMTALSVRYLAICRPLRARVLTNRVRLALIAVLWAVALLSAGPFLFL 176
Db 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFWIAVAFCSAGPIFVL 181
QY 177 VGEQDPGISVVGINGTARIASSPLASSPPLWLSRAPPPSPGPETAFAAALFSRBCR 236
Db 182 VGVHE-----NGT-----DP-W-----DTNECR 199
QY 237 PS--PAQLGALRWLVTTAYFFLPCLLSILYGLIGBELWSSRRPLRGPAASGRGHR 294
Db 200 PTEFAVRSGLLTVMWVSSIFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259
QY 295 QTVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
Db 260 QTVKMLAVVVFAPILCWLPFHVGRLYFSKSPGPSLEIAQISQYCNLVSVFLFYLSAIN 319
QY 352 PILYNLSKYYRAAFKLLARKSRPRGHRSDTAGVAGDTGGDTVGYTETSAN 407
Db 320 PILYNIMSKYRVAVFRLGPEFQSQRKSLTKDESSR-----AWTESSIN 365

RESULT 7
US-09-170-496D-88
/ Sequence 88, Application US/09170496D
/ Patent No. 6555339
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Liaw, Chen W.
/ TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
/ FILE OF INVENTION: Receptors
/ FILE REFERENCE: AREN-0040
/ CURRENT APPLICATION NUMBER: US/09/170,496D
/ CURRENT FILING DATE: 1998-10-13
/ NUMBER OF SEQ ID NOS: 294
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RESULT 11
US-09-743-475-4
; Sequence 4, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-743-475-4

Query Match      40.1%; Score 863.5; DB 4; Length 366;
Best Local Similarity 44.7%; Pred. No. 2,9e-66;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDGPEGA-----REPPWALPPCD-----ERRCSPPFGLGALVPVAVCLCLFVVGVSQN 56
DB 2 WNAETSEEPGNLTADLDWDASPGNDSLGDELLOLFPAPLIAGVTATCVALLFVVGIA 61

QY 57 VVTVMILGRYDRMTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPMVFGPLLCRLSLY 116
DB 62 LUTMLVVSFRERITTNLYLSMAFSDLLIFLCPLDLVRLWQYRPNFGLLCKLPQF 121

QY 117 VGECTYATLLHMTALSVERYLAICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLFL 176
DB 122 VSECTYATVLTITALSVERYFAICFPLRAKVVTIKGRVKLVIFVIAVAFCSAGPIFVL 181

QY 177 VGEQDPGISVVGPLNGTARIASSPLASSPPLWLRAPPPSPGPETAAALFSRECR 236
DB 182 VGVHEH-----NGT-----DP--W-----DTNECR 199

QY 237 PS--PAQLGALVLMVWTTTAYFELPLCLSLYGLIGRELWSSRRPLRGPAAASGRGRH 294
DB 200 PTEFAVRSGLLTVMWVSSIFFLPVFCUTVLYSLIGRLKWRRRRGDAVVGASLRDQNH 259

QY 295 QTVRVLVVLVLAFLICWLPFHVGRITTYINTEDS---RMMYFSQYFNIVALQLFYLSASIN 351
DB 260 QIVKMLAVVVFARILLWLPFHVGRYLFKSFEPSLEIAIQISQYCNLVSVFLFYLSA 319

QY 352 PILYNIISKYRAAFKLLARKSRPGRHRSRDTAGEVAGDTGDTVGYTETSAN 407
DB 320 PILYNIIMSKYRVAVPRLIGFEPFSQKSLTLKDESSR-----AWTESSIN 365

RESULT 12
US-09-077-675A-3
; Sequence 3, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H. T.
```

```
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-675A-3

Query Match      40.0%; Score 863; DB 3; Length 353;
Best Local Similarity 46.5%; Pred. No. 3e-66;
Matches 186; Conservative 53; Mismatches 95; Indels 66; Gaps 9;

QY 19 WPALPPCD---ERRCSPPFGLGALVPVAVCLCLFVVGVSQNVVWMLIGRVRDMRTTNL 75
DB 8 WDAPPENDSLVEELLPLPFTPLLAGVTATCVALLFVVGIAGNLLTMLVVSFRPREMTTNL 67

QY 76 YLGSMVSDLLILGLPFDLYRLWRSRPMVFGPLLCRLSLYVGECTYATLLHMTALSVE 135
DB 68 YLSSMAFSDLLIFLCPLDLFRLWQYRPNLGNLLCKLPQFVSECTYATVLTITALSVE 127

QY 136 RYLAICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLFVVGVDQDPGISVVGPLNGTA 195
DB 128 RYFALCFPLRAKVVTIKGRVKLVIVIAVAFCSAGPIFVLVGVHEH-----NGT- 177

QY 196 RIASSPLASSPPLWLRAPPPSPGPETAAALFSRECRPS---PAQLGALVLMVWTT 253
DB 178 -----DPRD-----TNECRATEFAVRSGLLTVMWVSS 205

QY 254 AYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASG---RERCHROTVRVLVVLVLAFLIC 310
DB 206 VFFFLPVFCLTVLYSLIGRKLW---RRKRGEAAVSGSSLRDQNHKQTVKMLAVVVFALIC 262

QY 311 WLPFHVGRITTY---INTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISKYRAAAF 367
DB 263 WLPFHVGRYLFKSFEPSLEIAIQISQYCNLVSVFLFYLSA 322

QY 368 KLLARKSRPGRHRSRDTAGEVAGDTGDTVGYTETSAN 407
DB 323 KLIGPEPFSQKSLTLKDESSR-----AWTESSIN 352

RESULT 13
US-09-077-674-3
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```
; Sequence 3, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,674
; FILING DATE: 3-JUN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19589P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-674-3

Query Match 40.0%; Score 863; DB 4; Length 353;
Best Local Similarity 46.5%; Pred. No. 3e-66;
Matches 186; Conservative 53; Mismatches 95; Indels 66; Gaps 9;

Qy 19 WPALPPCD---ERRCSPPPLGALVPVTAACLVGVGSGNVVTVMLIGRYVDMRTTNL 75
Db 8 WDAPPENDSLVEELLPLFPTELLAGVTATCVAFVVGAGNLLTMLVVSFRMRTTNL 67

Qy 76 YLGSMAVSDLLILGLPDLVRLWRSRPPVFGPLLCRLSLVVGECTVATLLHMTALSVE 135
Db 68 YLSSMAFSDLLIFLCMPDLDFRLWQYRPNWLNGLLCKLFQFVSESTVATVLTITALSVE 127

Qy 136 RYLAICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLVLGVQDPGISVVPGLNGTA 195
Db 128 RYFAICFPLRAKVVVTKGRVKLVILVIAVAFCSAGPIFVLGVGVEHD-----NGT- 177

Qy 196 RIASSPLASSPPLWLSRAPPPSPGPGPETAABALFSECRPS--PAQLGALRVMWMTT 253
Db 178 -----DPRD-----TNECRATEFAVRSGLLTVMVWVSS 205

Qy 254 AYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAAG---RRGRHQTVRVLLVWVLAFTIC 310
Db 206 VFFLPFLVCLTVLSLIGRKLW---RRKRGANVGSRLQDNHKTQVMKLVAVVFAFILC 262

Qy 311 WLPFHVGRIIY---INTEDSRMVFYSQYFNIVALQLFYLASINPILYNLISKYRAAAF 367

; Sequence 16, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-675A-16

Query Match 40.0%; Score 861.5; DB 3; Length 364;
Best Local Similarity 48.3%; Pred. No. 4.2e-66;
Matches 185; Conservative 52; Mismatches 81; Indels 65; Gaps 11;

Qy 5 WNGSDGPEGAREP-----PWPALPPCD---ERRCSPPPLGALVPVTAACLVGVGSG 55
Db 2 WNAAT--PSEPEPNTVLDLDWDASPGNDSLPDELLPLFPAPLLAGVTATCVAFVVGISG 59

Qy 56 NVTVMLIGRYVDMRTTNLYLGSMAVSDLLILGLPDLVRLWRSRPPVFGPLLCRLSL 115
Db 60 NLLTMLVVSFRMRTTNLYLSSMAFSDLLIFLCMPDLDFRLWQYRPNWLNGLLCKLFQ 119

Qy 116 YVGGCTVATLLHMTALSVERYLAICRPLRARVLTTRRRVRLIAVLWAVALLSAGPFLF 175
Db 120 FVSESTVATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVILVIAVAFCSAGPIFV 179

Qy 176 LVGVQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPGPETAABALFSECR 235
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Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197
Qy 236 RPS--PAQGLARVLMWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAG---RE 290
Db 198 RATEFAVRSGLLTVMWVSSVFFLPVFCLTLYSLIGRKLW--RR--RGDAAVGASLRD 253
Qy 291 RGHRTQVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMMYFSQYFNIVALQLFVLS 347
Db 254 QNHKQTVKMLAVVFAFICWLPFHVGRIYLFKSPGSLTAQISQYCNLVSVFLVLS 313
Qy 348 ASINPILYNLSKKYRAAAFKLL 370
Db 314 AAINPILYNIMSKKYRVAVFKLL 336

RESULT 15

US-09-077-674-16
; Sequence 16, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 B. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,674
; FILING DATE: 3-JUN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19589P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-077-674-16

Query Match 40.0%; Score 861.5; DB 4; Length 364;
Best Local Similarity 48.3%; Pred. No. 4.2e-66;
Matches 185; Conservative 52; Mismatches 81; Indels 65; Gaps 11;

Qy 5 WNGSDGREGAREP-----PWPALPPC-----ERRCSPEPLGALVPVTAVCLCLFVVGUSG 55
Db 2 WNAT--PSEEPFNVTLDWDASFGNDSLPDELLPLFPALLAGVTATCVALFVVGISG 59

Qy 56 NVVTMLIGRYDRMTTNNLYLGSWAYSDLLILGLPEDLYLWRSRPMVFGPLICRLSL 115
Db 60 NLLTMLVVSRRPRELRTTNNLYLSSMAFSDDLIFLCMLDLVRLWQYRPWNFGDLLCKLFQ 119
Qy 116 YVGBGCTYATLLHMTALTSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPPLF 175
Db 120 FVSESCIYATVLTITALSVERYPAICPLRAKVVVTKGRVKLVILVIWAVAFCSAGPIFV 179
Qy 176 LVGVEQDPGISVVPGLNGTARIASSPLASSPPLMLSRAPPPSPGPGTETAAAAALFSREC 235
Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197
Qy 236 RPS--PAQGLARVLMWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAG---RE 290
Db 198 RATEFAVRSGLLTVMWVSSVFFLPVFCLTLYSLIGRKLW--RR--RGDAAVGASLRD 253
Qy 291 RGHRTQVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMMYFSQYFNIVALQLFVLS 347
Db 254 QNHKQTVKMLAVVFAFICWLPFHVGRIYLFKSPGSLTAQISQYCNLVSVFLVLS 313
Qy 348 ASINPILYNLSKKYRAAAFKLL 370
Db 314 AAINPILYNIMSKKYRVAVFKLL 336

Search completed: April 11, 2005, 21:06:22
Job time : 23.1679 secs

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OM protein - protein search, using sw model

Run on: April 11, 2005, 21:05:05 ; Search time 236.977 Seconds
(without alignments)
577.198 Million cell updates/sec

Title: US-09-719-485-3
Perfect score: 2155
Sequence: 1 MGSPWNGSDGEGAREPPWP.....DTGGDTGVGYTTSANVKTMG 412

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2155	100.0	412	14	US-10-225-567A-473
2	2155	100.0	412	14	US-10-290-078-15
3	2155	100.0	412	14	US-10-318-661-28
4	2155	100.0	412	14	US-10-206-677-2
5	2149	99.7	412	10	US-09-876-252-130
6	2149	99.7	412	15	US-10-417-820A-130
7	2149	99.7	412	15	US-10-417-820A-150
8	2149	99.7	412	16	US-10-723-955-130
9	863.5	40.1	366	14	US-10-251-385-88
10	863.5	40.1	366	14	US-10-303-204A-13
11	863	40.0	353	14	US-10-303-204A-3
12	861.5	40.0	364	14	US-10-303-204A-16
13	860	39.9	361	14	US-10-303-204A-8

14	857.5	39.8	366	14	US-10-251-385-210	Sequence 210, Appl
15	775.5	36.0	302	14	US-10-303-204A-2	Sequence 2, Appl
16	774.5	35.9	302	14	US-10-303-204A-7	Sequence 7, Appl
17	674.5	31.3	271	14	US-10-303-204A-12	Sequence 12, Appl
18	644.5	29.9	289	14	US-10-225-567A-140	Sequence 140, Appl
19	644.5	29.9	289	14	US-10-303-204A-10	Sequence 10, Appl
20	633	29.4	289	14	US-10-303-204A-5	Sequence 5, Appl
21	501	23.2	424	16	US-10-915-157-7	Sequence 7, Appl
22	497	23.1	418	14	US-10-225-567A-207	Sequence 207, Appl
23	491	22.8	418	10	US-09-826-509-535	Sequence 535, Appl
24	491	22.8	418	17	US-10-925-095-535	Sequence 53, Appl
25	486.5	22.6	445	15	US-10-240-145-53	Sequence 53, Appl
26	486.5	22.6	445	15	US-10-240-145-139	Sequence 139, Appl
27	485.5	22.5	403	14	US-10-251-385-114	Sequence 114, Appl
28	485.5	22.5	403	14	US-10-225-567A-540	Sequence 540, Appl
29	485.5	22.5	403	14	US-10-290-078-18	Sequence 18, Appl
30	485.5	22.5	403	15	US-10-353-690-10	Sequence 10, Appl
31	485.5	22.5	403	16	US-10-915-157-8	Sequence 8, Appl
32	483.5	22.4	403	14	US-10-251-385-224	Sequence 224, Appl
33	483	22.4	415	16	US-10-203-015A-17	Sequence 17, Appl
34	483	22.4	415	17	US-10-890-407A-1	Sequence 1, Appl
35	479	22.2	412	16	US-10-770-583-8	Sequence 8, Appl
36	479	22.2	415	16	US-10-770-583-6	Sequence 6, Appl
37	479	22.2	415	17	US-10-215-619-2	Sequence 2, Appl
38	477.5	22.2	395	15	US-10-258-423-6	Sequence 6, Appl
39	477.5	22.2	396	15	US-10-258-423-8	Sequence 8, Appl
40	476	22.1	402	15	US-10-258-423-4	Sequence 4, Appl
41	476	22.1	412	14	US-10-225-567A-557	Sequence 557, Appl
42	476	22.1	412	16	US-10-770-583-4	Sequence 4, Appl
43	476	22.1	415	10	US-09-875-076-12	Sequence 12, Appl
44	476	22.1	415	10	US-09-876-252-12	Sequence 12, Appl
45	476	22.1	415	14	US-10-272-983-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-10-225-567A-473
; Sequence 473, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225.567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 473
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-473

Query Match	100.0%	Score	2155;	DB	14;	Length	412;
Best Local Similarity	100.0%	Pred. No.	2.6e-167;				
Matches	412;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MGSPWNGSDGEGAREPPWPALPCDDERRCSPFPLGALVPVTAVCLCLFVVGVSQNVTV	60				
Db	1	MGSPWNGSDGEGAREPPWPALPCDDERRCSPFPLGALVPVTAVCLCLFVVGVSQNVTV	60				
Qy	61	MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSPWVFGPLLCRLSLYVGE	120				
Db	61	MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSPWVFGPLLCRLSLYVGE	120				
Qy	121	CTYATLLHMTALSVERYLAIICRLRARVLTTRRRVRLIAVLMAVALLSAGPFLVGV	180				

Db 121 CYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180
QY 181 QPGLISVPLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
Db 181 QPGLISVPLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300
Db 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300
QY 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360
Db 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360
QY 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTMG 412
Db 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTMG 412

RESULT 2

US-10-290-078-15
; Sequence 15, Application US/10290078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: 14395, 14618, 17692 or 58874
; FILE REFERENCE: MPI2001-288P1(M)
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-078-15

Query Match 100.0%; Score 2155; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPEGAREPPWLPALPPCDERRCSPPLGALVPVTVAVCLCLFVVGVSNGVTV 60
Db 1 MGSPWNGSDGPEGAREPPWLPALPPCDERRCSPPLGALVPVTVAVCLCLFVVGVSNGVTV 60
QY 61 MLIGRYDRMRTTNNLYGSMVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLYVGBG 120
Db 61 MLIGRYDRMRTTNNLYGSMVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLYVGBG 120
QY 121 CYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180
Db 121 CYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180
QY 181 QPGLISVPLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
Db 181 QPGLISVPLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300
Db 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300
QY 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360
Db 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360
QY 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTMG 412
Db 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTMG 412

RESULT 3

US-10-318-661-28
; Sequence 28, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-661-28

Query Match 100.0%; Score 2155; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPEGAREPPWLPALPPCDERRCSPPLGALVPVTVAVCLCLFVVGVSNGVTV 60
Db 1 MGSPWNGSDGPEGAREPPWLPALPPCDERRCSPPLGALVPVTVAVCLCLFVVGVSNGVTV 60
QY 61 MLIGRYDRMRTTNNLYGSMVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLYVGBG 120
Db 61 MLIGRYDRMRTTNNLYGSMVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLYVGBG 120
QY 121 CYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180
Db 121 CYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVGE 180
QY 181 QPGLISVPLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
Db 181 QPGLISVPLNGTARIASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300
Db 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRL 300
QY 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360
Db 301 LVVLAFTICWLPFFHVGRIIYINTEDSRMYFSQYFNIVALQLFYLSASINPILYNLISK 360
QY 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTMG 412
Db 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGDTGVYTTTSANVKTMG 412

RESULT 4

US-10-206-677-2
; Sequence 2, Application US/10206677
; Publication No. US20030186336A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences, Inc.
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; APPLICANT: Kulaender, Bruce G.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO
; TITLE OF INVENTION: GPCR 38, A G PROTEIN-COUPLED RECEPTOR (GPCR)
; FILE REFERENCE: 1920-1-8
; CURRENT APPLICATION NUMBER: US/10/206,677

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; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/250,251
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,452
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-206-677-2

Query Match      100.0%; Score 2155; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCCLFVVGVSGNVTV 60
DB 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCCLFVVGVSGNVTV 60
QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPGLLCRLSLYVGE 120
DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPGLLCRLSLYVGE 120
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180
DB 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180
QY 181 QDPGIVVPGNGTARIASSPLASSPPLWLSRAPPPSPGPETAABAAALFSRECRPSPA 240
DB 181 QDPGIVVPGNGTARIASSPLASSPPLWLSRAPPPSPGPETAABAAALFSRECRPSPA 240
QY 241 QLGLRVLMLVWTTATFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASRGHRGRTVRL 300
DB 241 QLGLRVLMLVWTTATFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASRGHRGRTVRL 300
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFYSQYFNIVALQLFYLSASINPILYNLSK 360
DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMVFYSQYFNIVALQLFYLSASINPILYNLSK 360
QY 361 KYRAAFKLLARKSRPRGFRHSRTAGEVAGDTGGDTGVGTETTSANVKTWG 412
DB 361 KYRAAFKLLARKSRPRGFRHSRTAGEVAGDTGGDTGVGTETTSANVKTWG 412

RESULT 5
US-09-876-252-130
; Sequence 130, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26

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; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 130
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-130

Query Match      99.7%; Score 2149; DB 10; Length 412;
Best Local Similarity 99.8%; Pred. No. 7.9e-167;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCCLFVVGVSGNVTV 60
DB 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCCLFVVGVSGNVTV 60
QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPGLLCRLSLYVGE 120
DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPGLLCRLSLYVGE 120
QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180
DB 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180

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QY 181 QDPGIVVPLGNTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
 DB 181 QDPGIVVPLGNTARIASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
 QY 241 QLGALRVLWMTTAYFFFLPCLSLYGLIGRELWSSRRPLRGPAAASGRGRHRTQTVRL 300
 DB 241 QLGALRVLWMTTAYFFFLPCLSLYGLIGRELWSSRRPLRGPAAASGRGRHRTQTVRL 300
 QY 301 LVVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
 DB 301 LVVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
 QY 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412
 DB 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412

RESULT 6

US-10-417-820A-130
 ; Sequence 130, Application US/10417820A
 ; Publication No. US20030229216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lowitz, Kevin
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Behan, Dominic P.
 ; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
 ; FILE REFERENCE: 7.US28.CON
 ; CURRENT APPLICATION NUMBER: US/10/417,820A
 ; CURRENT FILING DATE: 2003-04-16
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; PRIOR APPLICATION NUMBER: 60/110,060
 ; PRIOR FILING DATE: 1998-11-27
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,852
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/109,213
 ; PRIOR FILING DATE: 1998-11-20
 ; PRIOR APPLICATION NUMBER: 60/123,944
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,945
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,948
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,951
 ; PRIOR FILING DATE: 1999-03-12
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 155
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 130
 ; LENGTH: 412
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-417-820A-130

Query Match 99.7%; Score 2149; DB 15; Length 412;
 Best Local Similarity 99.8%; Pred. No. 7.9e-167;
 Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGSPWNGSDGPEGAREPPWLPALPPCDERRCSPFFPLGALVPVTAVALCLFVVGSGNVTV 60
 DB 1 MGSPWNGSDGPEGAREPPWLPALPPCDERRCSPFFPLGALVPVTAVALCLFVVGSGNVTV 60
 QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120
 DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVERYLAIICRPLRARVLVTRRRVRALIAVLWALLSAGPFFFLVGVE 180
 DB 121 CTYATLLHMTALSVERYLAIICRPLRARVLVTRRRVRALIAVLWALLSAGPFFFLVGVE 180
 QY 181 QDPGIVVPLGNTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
 DB 181 QDPGIVVPLGNTARIASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
 QY 241 QLGALRVLWMTTAYFFFLPCLSLYGLIGRELWSSRRPLRGPAAASGRGRHRTQTVRL 300
 DB 241 QLGALRVLWMTTAYFFFLPCLSLYGLIGRELWSSRRPLRGPAAASGRGRHRTQTVRL 300
 QY 301 LVVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
 DB 301 LVVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
 QY 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412
 DB 361 KYRAAFKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412

RESULT 7

US-10-417-820A-150
 ; Sequence 150, Application US/10417820A
 ; Publication No. US20030229216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lowitz, Kevin
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Behan, Dominic P.
 ; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
 ; FILE REFERENCE: 7.US28.CON
 ; CURRENT APPLICATION NUMBER: US/10/417,820A
 ; CURRENT FILING DATE: 2003-04-16
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; PRIOR APPLICATION NUMBER: 60/110,060
 ; PRIOR FILING DATE: 1998-11-27
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,852
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/109,213
 ; PRIOR FILING DATE: 1998-11-20
 ; PRIOR APPLICATION NUMBER: 60/123,944
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,945
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,948
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,951
 ; PRIOR FILING DATE: 1999-03-12
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 155
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 150
 ; LENGTH: 412
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-417-820A-150

Query Match 99.7%; Score 2149; DB 15; Length 412;
 Best Local Similarity 99.8%; Pred. No. 7.9e-167;
 Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGSPWNGSDGPEGAREPPWLPALPPCDERRCSPFFPLGALVPVTAVALCLFVVGSGNVTV 60
 DB 1 MGSPWNGSDGPEGAREPPWLPALPPCDERRCSPFFPLGALVPVTAVALCLFVVGSGNVTV 60

QY 61 MLIGRYDMRTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120
DB 61 MLIGRYDMRTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120
QY 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGV 180
DB 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGV 180
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
QY 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERHGRQTQKVL 300
DB 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERHGRQTQKVL 300
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
QY 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412
DB 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412

RESULT 8

US-10-723-955-130
; Sequence 130, Application US/10723955
; Publication No. US20040110238A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lehman-Bruinsma, Karin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Gore, Martin
; APPLICANT: White, Carol
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US29.CON
; CURRENT APPLICATION NUMBER: US/10/723,955
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 10/417,820
; PRIOR FILING DATE: 2003-4-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-723-955-130

Query Match 99.7%; Score 2149; DB 16; Length 412;
Best Local Similarity 99.8%; Pred. No. 7.9e-167;
Matches 411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPPFPGALVPVTAIVCLCLFVVGVSGNVTV 60
DB 1 MGSPWNGSDGPEGAREPPWALPCDERRCSPPFPGALVPVTAIVCLCLFVVGVSGNVTV 60
QY 61 MLIGRYDMRTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120
DB 61 MLIGRYDMRTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120
QY 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGV 180
DB 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGV 180
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRPSA 240
QY 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERHGRQTQKVL 300
DB 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRERHGRQTQKVL 300
QY 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
DB 301 LVVLAFTICWLPFHVGRIIYINTEDSRMMYFSQYFNIVALQLFYLSASINPILYNLISK 360
QY 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412
DB 361 KYRAAFAKLLARKSRPRGFRHSRDTAGEVAGDTGGDTVGYTETSANVKTWG 412

RESULT 9

US-10-251-385-88
; Sequence 88, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-88

Query Match 40.1%; Score 863.5; DB 14; Length 366;
Best Local Similarity 44.7%; Pred. No. 4.2e-62;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;
QY 5 WNGSDGPEGA----REPPWALPPCD---ERRCSPPFPGALVPVTAIVCLCLFVVGVSGN 56
DB 2 WNATPSEBPGNLTADLDWDASFGNDSGLDELQLFPAPLAGVTATCVAFVVGIGAGN 61
QY 57 VVTVMILIGRYDMRTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLY 116
DB 62 LITMLVWSRPRELRTTNNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPNWFGDLCKLQF 121
QY 117 VEGCTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFL 176


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Db 122 VSECTYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVIFVIWAVFAGSAGPIFVL 181
QY 177 VGVQDPGIVSVVGLNGTARIASSPLASSPPLWLRAPPPSPGPETAABAAALFSRECR 236
Db 182 VGVHEH-----NGT-----DP--W-----DTNECR 199
QY 237 PS--PAQLGALRVMLVVTAYFFLPCLISILYGLIGRELWSSRRPLRGPAAAGRGRHR 294
Db 200 PTEFAVRSGLLTVWVWSSIEFFLPVCLTVLSIGRKLWRRRGDVAVGASLDDQNHK 259
QY 295 QTVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
Db 260 QTVKMLAVVVFALICWLPFHVGRLFSKSPGSLTAQISQYCNLVSVFLFYLAAIN 319
QY 352 PLYNLISKYRAAFAKLLARKSRPGRFHRSDRTAGEVAGDTGGDTVGYTETSAN 407
Db 320 PLYNIMSKYRAVAVFRLGFPFSGRKLSTLKDESSR-----AWTESSIN 365

RESULT 10
US-10-303-204A-13
; Sequence 13, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR FILING DATE: 1996-018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 366
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-303-204A-13

Query Match 40.1%; Score 863.5; DB 14; Length 366;
Best Local Similarity 44.7%; Pred. No. 4.2e-62;
Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

QY 5 WNGSDQPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTVACLCIFVVGSGN 56
Db 2 WNAFSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATCVALFVVGAGN 61
QY 57 VTVMLIGRYDRMTTNLYLGSMAVSDLLILGLPFDLYLRWSRPVWFGPCLLCRLSLY 116
Db 62 LUTMLVSRFRELRTTNLYLSSMAFSDLLIFLCMPDLVRLQVYRPNWFGDLCFLQF 121
QY 117 VCEGCTYATLLHWTALSVERYLAICRPLARVLTTRRRVRLIAVLWALLSAGPFLFL 176
Db 122 VSECTYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVIFVIWAVFAGSAGPIFVL 181
QY 177 VGVQDPGIVSVVGLNGTARIASSPLASSPPLWLRAPPPSPGPETAABAAALFSRECR 236
Db 182 VGVHEH-----NGT-----DP--W-----DTNECR 199
QY 237 PS--PAQLGALRVMLVVTAYFFLPCLISILYGLIGRELWSSRRPLRGPAAAGRGRHR 294

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Db 200 PTEFAVRSGLLTVWVWSSIEFFLPVCLTVLSIGRKLWRRRGDVAVGASLDDQNHK 259
QY 295 QTVRVLLVVLAFIICWLPFHVGRIIYINTEDS---RMVFSQYFNIVALQLFYLSASIN 351
Db 260 QTVKMLAVVVFALICWLPFHVGRLFSKSPGSLTAQISQYCNLVSVFLFYLAAIN 319
QY 352 PLYNLISKYRAAFAKLLARKSRPGRFHRSDRTAGEVAGDTGGDTVGYTETSAN 407
Db 320 PLYNIMSKYRAVAVFRLGFPFSGRKLSTLKDESSR-----AWTESSIN 365

RESULT 11
US-10-303-204A-3
; Sequence 3, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR FILING DATE: 1996-018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-3

Query Match 40.0%; Score 863; DB 14; Length 353;
Best Local Similarity 46.5%; Pred. No. 4.4e-62;
Matches 186; Conservative 53; Mismatches 95; Indels 66; Gaps 9;

QY 19 WPALPPCD---ERRCSPFPLGALVPVTVACLCIFVVGSGNVVTVMLIGRYDRMTTNL 75
Db 8 WDAPPENDSLVEELLPLFPPTLAGVATCVALFVVGAGNLLTLMVVSFRERMTTNL 67
QY 76 YLGSMAVSDLLILGLPFDLYLRWSRPVWFGPCLLCRLSLYVVGCTYATLLHWTALSVE 135
Db 68 YLSSMAFSDLLIFLCMPDLVRLQVYRPNWFGPCLLCRLSLYVVGCTYATLLHWTALSVE 127
QY 136 RYLAICRPLARVLTTRRRVRLIAVLWALLSAGPFLFLVGVQDPGIVSVVFLNGTA 195
Db 128 RYFAICRPLARVLTTRRRVRLIAVLWALLSAGPFLFLVGVQDPGIVSVVFLNGTA 177
QY 196 RIASSPLASSPPLWLRAPPPSPGPETAABAAALFSRECRPS--PAQLGALRVMLVWTT 253
Db 178 -----DPRD-----TNECEATFAVRSGLLTVWVWSS 205
QY 254 AYFFLPCLISILYGLIGRELWSSRRPLRGPAAAGS---RRGHRQTVRVLLVVLAFIIC 310
Db 206 VFFLPVCLTVLSIGRKLW---RRKRGAAVGSLLRDNHKTQVTKMLAVVVFALIC 262
QY 311 WLPFHVGRIIY---INTEDSRMVFYFNIVALQLFYLSASINPILYNLISKYRAAAF 367
Db 263 WLPFHVGRIYFSLKSPGSEVIEIAQISQYCNLVSVFLFYLAAINPILYNLISKYRAAF 322

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QY 368 KLLARKSPRGHRSRDTAGEVAGDTGDTGVGTETSAN 407
 Db 323 KLLGFEPFSQKSLTLKDESSR-----AWTESSIN 352

RESULT 12

US-10-303-204A-16
 ; Sequence 16, Application US/10303204A
 ; Publication No. US20030166144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Arena, Joseph P.
 ; APPLICANT: Cully, Doris F.
 ; APPLICANT: Feighner, Scott D.
 ; APPLICANT: Howard, Andrew D.
 ; APPLICANT: Liberator, Paul A.
 ; APPLICANT: Schaeffer, James M.
 ; APPLICANT: Van Der Ploeg, Leonardus H. T.
 ; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
 ; TITLE OF INVENTION: FAMILY

; FILE REFERENCE: 19589PCA
 ; CURRENT APPLICATION NUMBER: US/10/303,204A
 ; CURRENT FILING DATE: 2002-11-25
 ; PRIOR APPLICATION NUMBER: 09/077,674
 ; PRIOR FILING DATE: 1998-06-03
 ; PRIOR APPLICATION NUMBER: PCT/US96/19445
 ; PRIOR FILING DATE: 1996-12-10
 ; PRIOR APPLICATION NUMBER: 60/018,962
 ; PRIOR FILING DATE: 1996-06-06
 ; PRIOR APPLICATION NUMBER: 60/008,582
 ; PRIOR FILING DATE: 1995-12-13
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: rattus norvegicus

US-10-303-204A-16

Query Match 40.0%; Score 861.5; DB 14; Length 364;
 Best Local Similarity 48.3%; Pred. No. 6.1e-62;
 Matches 185; Conservative 52; Mismatches 81; Indels 65; Gaps 11;

QY 5 WNGSGPEGARP-----PWALPPCD-----ERRCSPPPLGALVPVTAVCLCLFVVGSG 55
 Db 2 WNAT--PSEEPFNVTLDLDWDASPGNDSLDELPLFPAPLAGVTATCVAFVVGISG 59
 QY 56 NVVTVMILGRYDRMTTNLXGSMVAVSDLLILGLPDLVLRWSRPWVFGPPLCRLSL 115
 Db 60 NLTWMLVSRFRELRTTNLYLSSWAFSDLLIFLCMPDLVLRWQYRPWNFGDLCKLPQ 119
 QY 116 YVGECTYATLHMTALSVERYLAICRPLRVLVTRRRVRLIALVMAVALLSAGPELF 175
 Db 120 FVSECTYATVLTITALSVERYFAICPLRAKVVTKGRVKLVILVIAWAFCSAGPIFV 179
 QY 176 LVGEQDQGISVVPGLNGTARTIASSPLASSPPLWLSRAPPPSPGPGTAAALFSREC 235
 Db 180 LVGVEHE-----NGT-----DPRD-----TNEC 197
 QY 236 RPS--PAQGLARVLMWTTAYFFLPFLCLSLYLGLIGRELWSSRRPLRGPASG--RE 290
 Db 198 RATEFAVRSGLLTVMVSSVFFFLVFLVTLVLSLGRKLM--RR--RGDAAVGASLRD 253
 QY 291 RGHQTVRLVLLVVLAFIACMLPPHVGRIIYINTEDS---RMVFSQYFNIVALOLFVLS 347
 Db 254 QNHQTVKMLAVVVFALFCLWLPFHVGRYLFSPGSEFSGLEIAQISQYCNLVSFVLVLS 313
 QY 348 ASINPILYNLSKKYRAAFKLL 370
 Db 314 AAINPILYNLSKKYRVAVFKLL 336

RESULT 13

US-10-303-204A-8

; Sequence 8, Application US/10303204A
 ; Publication No. US20030166144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Arena, Joseph P.
 ; APPLICANT: Cully, Doris F.
 ; APPLICANT: Feighner, Scott D.
 ; APPLICANT: Howard, Andrew D.
 ; APPLICANT: Liberator, Paul A.
 ; APPLICANT: Schaeffer, James M.
 ; APPLICANT: Van Der Ploeg, Leonardus H. T.
 ; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
 ; TITLE OF INVENTION: FAMILY

; FILE REFERENCE: 19589PCA
 ; CURRENT APPLICATION NUMBER: US/10/303,204A
 ; CURRENT FILING DATE: 2002-11-25
 ; PRIOR APPLICATION NUMBER: 09/077,674
 ; PRIOR FILING DATE: 1998-06-03
 ; PRIOR APPLICATION NUMBER: PCT/US96/19445
 ; PRIOR FILING DATE: 1996-12-10
 ; PRIOR APPLICATION NUMBER: 60/018,962
 ; PRIOR FILING DATE: 1996-06-06
 ; PRIOR APPLICATION NUMBER: 60/008,582
 ; PRIOR FILING DATE: 1995-12-13
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 361
 ; TYPE: PRT
 ; ORGANISM: homo sapiens

US-10-303-204A-8

Query Match 39.9%; Score 860; DB 14; Length 361;
 Best Local Similarity 46.1%; Pred. No. 8e-62;
 Matches 183; Conservative 57; Mismatches 97; Indels 60; Gaps 8;

QY 19 WPALPPCD-----ERRCSPPPLGALVPVTAVCLCLFVVGSGNVVTVMILGRYDRMTTNL 75
 Db 16 WDASPGNDSLGLDELQLFPAPLAGVTATCVAFVVGIAGNLLTMLVSVRFRELRTTNL 75
 QY 76 YLGSMAVSDLLILGLPDLVLRWSRPWVFGPPLCRLSLYVGECTYATLHMTALSVE 135
 Db 76 YLSSWAFSDLLIFLCMPDLVLRWQYRPWNFGDLCKLPQVSECTYATVLTITALSVE 135
 QY 136 RYLAICRPLRVLVTRRRVRLIALVMAVALLSAGPELFVLGVQDQGISVVPGLNGTA 195
 Db 136 RYFAICPLRAKVVTKGRVKLVIFVIAWAFCSAGPIFVLGVGEHE-----NGT- 185
 QY 196 RIASSPLASSPPLWLSRAPPPSPGPGTAAALFSRECRPS--PAQGLARVLMWTT 253
 Db 186 -----DP--W-----DTNECRPTEPAVRSGLLTVMVSS 213
 QY 254 AYFFLPFLCLSLYLGLIGRELWSSRRPLRGPASGRBGRHQTVRVLLVVLAFIICWLP 313
 Db 214 IFFLPFVCLVTLVSLIGRKLWRRRGDAVVGASURDQNHQTVKMLAVVVFALFCLWLP 273
 QY 314 FHVGRIIYINTEDS---RMVFSQYFNIVALOLFVLSASINPILYNLSKKYRAAFKLL 370
 Db 274 FHVGRYLFSPGSEFSGLEIAQISQYCNLVSFVLVLSAIPILYNLSKKYRVAVFKLL 333
 QY 371 LARKSRPGRFHRSDRTAGEVAGDTGGDTGVGTETSAN 407
 Db 334 GFEPFSQKSLTKDESSR-----AWTESSIN 360

RESULT 14

US-10-251-385-210
 ; Sequence 210, Application US/10251385
 ; Publication No. US20030105292A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P.
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G

```
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 210
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-210

Query Match      39.8%; Score 857.5; DB 14; Length 366;
Best Local Similarity 44.5%; Pred. No. 1.3e-61;
Matches 185; Conservative 59; Mismatches 107; Indels 65; Gaps 9;

QY  5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTAACLCLFVVGVSGN 56
DB  2 WNAFSEBPGFNLTLADLDWDASPNDSLGDELLQLFPAPLLAGVTATCVLFVVGIAGN 61

QY  57 VVTMLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPMWFGELLCRLSLY 116
DB  62 LLTMLVSRFRRLTNNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLQF 121

QY  117 VQEGCTATLLHMTALSVERYLAICRPLARVLTTRRRVRLIALVLAVALLSAGPFLFL 176
DB  122 VSSECTATVLTALSVERYFAICFPLRAKVVVTKGRVKLVIFVIMAVAFCSAGPIFVL 181

QY  177 VQVEODPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECR 236
DB  182 VQVEHE-----NGT-----DP--W-----DTNECR 199

QY  237 PS--PAQLGALRVMLWVTYAYFFLPCLSLYGLIGRELWSSRPLRGPAASGRERGHR 294
DB  200 PTEFAVRSGLLAVMVVSSVFFLPVCLTVLSYGLIGRELWSSRPLRGPAASGRERGHR 259

QY  295 QTVRVLLVVLAFIICWLPFHVGRIIYNTEDS---RMVFSQYFNIVALQLFVLSASIN 351
DB  260 QTKGMLAVVVFAPILCWLPHVGRYLFPSKSLPESGVEIAQISQYCNLVSVFLFVLSA 319

QY  352 PILYNLSKKYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTVGYTETSAN 407
DB  320 PILYNMSKKYRVAVFRLIGPFPFSQKSLTKDESSR-----AWTESSIN 365

RESULT 15
US-10-303-204A-2
; Sequence 2, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; TITLE OF INVENTION: FAMILY
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 302
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-2

Query Match      36.0%; Score 775.5; DB 14; Length 302;
Best Local Similarity 46.6%; Pred. No. 5e-55;
Matches 166; Conservative 48; Mismatches 79; Indels 63; Gaps 8;

QY  60 VMLIGRYDMRTTNNLYLGSMAVSDLLILLGLPFDLYRLWRSRPMWFGELLCRLSLY 119
DB  1 MLVVSRFRRLTNNLYLSSMAFSDLLIFLCMPDLFRLWQYRPNWNLGNLCKLQFVSE 60

QY  120 GCTVATLLHMTALSVERYLAICRPLARVLTTRRRVRLIALVLAVALLSAGPFLFLGV 179
DB  61 SCTVATVLTITLALSVERYFAICFPLRAKVVVTKGRVKLVILVIMAVAFCSAGPIFVL 120

QY  180 BODPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPS- 238
DB  121 EHD-----NGT-----DPRD-----TNECRATE 138

QY  239 -PAQLGALRVMLWVTYAYFFLPCLSLYGLIGRELWSSRPLRGPAASG---RERGHR 294
DB  139 FAVRSGLLTVMVVSSVFFLPVCLTVLSYGLIGRELWSSRPLRGPAASG---RERGHR 195

QY  295 QTVRVLLVVLAFIICWLPFHVGRIIY---INTEDSRMMYFSQYFNIVALQLFVLSASIN 351
DB  196 QTVKMLAVVVFAPILCWLPHVGRYLFPSKSLPESGVEIAQISQYCNLVSVFLFVLSA 255

QY  352 PILYNLSKKYRAAFAKLLARKSRPRGFHRSRDTAGEVAGDTGDTVGYTETSAN 407
DB  256 PILYNMSKKYRVAVFRLIGPFPFSQKSLTKDESSR-----AWTESSIN 301

Search completed: April 11, 2005, 21:21:24
Job time : 237.977 secs
```

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: April 11, 2005, 19:24:50 ; Search time 17.5539 Seconds
(without alignments)
2258.264 Million cell updates/sec

Title: US-09-719-485-3

Perfect score: 2155

Sequence: 1 MGSPWNGSDGEGAREPPWP.....DTGGDTGVGTTSANVTMG 412

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	23.2	424	2	JH0164
2	497	23.1	418	2	S29506
3	453	21.0	477	2	JC7913
4	437	20.3	418	2	A88013
5	420	19.5	595	2	JC8012
6	401	18.6	416	2	S68822
7	392	18.2	658	2	JC8011
8	375	17.4	378	2	T15816
9	359	16.7	363	2	I57940
10	357.5	16.6	418	2	A46226
11	344	16.0	363	2	I57955
12	344	16.0	364	2	JN0763
13	343.5	15.9	380	2	A55259
14	339	15.7	352	2	JE0296
15	339	15.7	380	2	S36143
16	335	15.5	380	2	JC2338
17	335	15.5	388	2	JN0605
18	334.5	15.5	367	2	JC2421
19	334.5	15.5	367	2	I49022
20	334.5	15.5	367	2	I56520
21	334.5	15.5	428	2	S30508
22	331.5	15.4	428	2	A44021
23	330.5	15.3	370	2	S43087
24	329	15.3	380	2	A48227
25	328	15.2	380	2	JC2434
26	327.5	15.2	384	2	A47249
27	326.5	15.2	372	2	I38532
28	326	15.1	519	2	S17783
29	322	14.9	384	2	JC4629

30 321.5 14.9 372 2 S34592 delta opioid recep
31 321.5 14.9 398 2 JN0708 thyrotropin-releas
32 320 14.8 372 2 B48227 delta opioid recep
33 319.5 14.8 387 2 JC5949 galanin receptor 2
34 318 14.8 411 2 I56444 thyrotropin-relea
35 318 14.8 412 2 S23436 thyroliberin recep
36 317 14.7 380 2 I38435 angiotensin recep
37 317 14.7 393 2 A39251 thyrotropin-releas
38 316 14.7 398 1 JQ1059 neurokinin 2 recep
39 315 14.6 391 2 C41795 somatostatin recep
40 312 14.5 373 2 JE0087 delta opioid recep
41 312 14.5 407 2 S23510 neurokinin 1 recep
42 311 14.4 391 2 A39297 somatostatin recep
43 311 14.4 407 1 JQ1274 neurokinin 1 recep
44 310 14.4 384 1 S00516 neurokinin 2 recep
45 310 14.4 407 2 A34357 neurokinin 1 recep

ALIGNMENTS

RESULT 1
JH0164

neurotensin receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: JH0164

R:Tanaka, K.; Masu, M.; Nakanishi, S.

Neuron 4, 847-854, 1990

A:Title: Structure and functional expression of the cloned rat neurotensin receptor.

A:Reference number: JH0164; MUID:90297956; PMID:1694443

A:Accession: JH0164

A:Molecule type: mRNA

A:Residues: 1-424 <TAN>

A:Cross-references: UNIPROT:P20789

C:Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor. The
ter (neurotensin) in the brain and as a hormone) cellular mediator in peripheral tiss

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

F:65-87/Domain: transmembrane #status predicted <TM1>

F:97-121/Domain: transmembrane #status predicted <TM2>

F:144-165/Domain: transmembrane #status predicted <TM3>

F:189-210/Domain: transmembrane #status predicted <TM4>

F:236-260/Domain: transmembrane #status predicted <TM5>

F:303-330/Domain: transmembrane #status predicted <TM6>

F:348-372/Domain: transmembrane #status predicted <TM7>

F:4,38,42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.2%; Score 501; DB 2; Length 424;
Best Local Similarity 32.9%; Pred. NO. 1.5e-32;
Matches 125; Conservative 59; Mismatches 110; Indels 86; Gaps 11;

QY 39 VPVTAVCLCLFVVGSGNVVTVMLIGR---YRDMRTTNLYLGSMVSDLLI-LIGLPPD 94
DB 65 VLVTAYIALFVVGTVGNSVTAFTLARKKSLQSLQSTVHYHLGSLALSDLLILLAMPVE 124
QY 95 LYR-LWRSRPVWFGPCLRLSLYVGEGETATLHMTALSVERYLAI CRPLARVLVTRR 153
DB 125 LYNFIWVHPWAFGDAGCGYFFLDADCTATALNVASLSVERYLAI CHPPKAKTLMRSR 184
QY 154 RVRALIAVLWAVALLSAGFFFLVGVGEODPGISVVVGLNGTARTIASSPLASSPPLWLSRA 213
DB 185 RTKKFISAILWLASALLAIPMLFTMGLQNRSGDTHPG-----GLVCTPIVDI----- 231
QY 214 PPPPPSPFETAEAAALFSPRCRSPAQLGALRVLWLTWTAYFFEL-PELCISILYGLIGR 272
DB 232 -----ATVKVQVNTFMSFLFFMLVILMTVIAN 262
QY 273 ELWSSRRPLRGPAASGR-----ERGHRTVTR-----VLLVVLVLAFTI 309
DB 263 KLTWM---VHQAEQGRVCTVGTGTHNGLEHSTFNMTIEGRVQALRHGVLVLEAVVAFV 319
QY 310 CWLPFFHVGRITIIYNTEDSR-----MMYFSQYFNIVALQLFYLSASINPILYNLISKYRAA 365


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Db 142 KIFSLWRANVLIIIAWTISFVCLPIPIAFIVQINKLPLPEDAKYQPTWKNKVSFFAVGVLN 201
Qy 204 SSPLWLGRAPPPSPGPETAEEAALFSREC-----RPSAQLGALRVMLVTTTAYFFL 258
Db 202 -----NRIPVVS-----TDGIFVLHTEFCAMNQSRPDQKM-----IIIFATVFFVI 244
Qy 259 PFLCLSLYGLIGRELWSSRRPLRGP--AASGRGRHQTQVRLVLLVVLAFIICWLPFHV 316
Db 245 PAIAIVIMYAHIAVLESSEIDLKGDQWVKRKNKSNRTVLKWLSSVITTFICWLPFHI 304
Qy 317 GRIIIVNTEDSRMVFQSFVNFVALQLFVLS-----ASINPILYNLISKYRAAAPKL 369
Db 305 QLLSVYTTWSETTISPPVQLSMIVFIYSFCYNSAANPILYNILSQIRSAFCRT 364
Qy 370 LL 371
Db 365 IL 366

RESULT 5
Jc8012
G protein-coupled neuropeptide pyrokinin-2 receptor (CG8795) - fruit fly (Drosophila mel)
C:Species: Drosophila melanogaster
C>Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C:Accession: Jc8012
R:Rosenkilde, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; DeLotto, R.
Biochem. Biophys. Res. Commun. 309, 485-494, 2003
A:Title: Molecular cloning, functional expression, and gene silencing of two Drosophila
A:Reference number: Jc8011; PMID: 12951076
A:Accession: Jc8012
A:Molecule type: mRNA
A:Residues: 1-595 <ROS>
A:CROSS-references: GB:AY277899
C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as
e. feeding, and behavior.
C:Genetics:
A:Gene: CG8795
A:introns: 115/1; 170/2; 214/3; 281/1; 352/3; 390/3
C:Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 19.5%; Score 420; DB 2; Length 595;
Best Local Similarity 29.7%; Pred. No. 6.4e-26;
Matches 121; Conservative 62; Mismatches 137; Indels 88; Gaps 13;

Qy 34 PLGALVPVTVAVCLCLFVGVSGNVVTVMLIGRYDRDMRTTNLGLGMAVSDLLILL-GLP 92
Db 58 PLSLLATLSVGVALLFIAGVLGNLITCIVISNNFWHTATNPLYLNLAISSDMLILCSGP 117
Qy 93 FDLYLRSPRVWFGPLICRLSLYVGECTYATLHMTALSVERYLAIICRPLRARVLVTR 152
Db 118 QDLYNLHPNDNYPFSDSICILSVLSEATANATVLTITAFVRYAICHPPRQHTMSKL 177
Qy 153 RRVALIAVLAVALLSAGPFLFVGVQDPCGISVVPGLNGTARTASPLASSPPLMLSR 212
Db 178 SRVAKFIFAIWAALLALPOAIFQSV-----VMQGTGCTCKNDFFAH----- 222
Qy 213 APPPPSPGPETAEEAALFSRECRPSAQLGALRVMLVTTTAYFFL--PFLCLSLYGLI 270
Db 223 -----VFVSGFLFPGGPMTAICVLYVLI 246
Qy 271 GRELMSSR--RPL-----RGAASGRGRHQTQVRLVLLVVLAFIICWLPFHVGRIRI- 319
Db 247 GVKLKRSLLQALPRCYDVNRGISAQTR-----VIRMLVAVAVAFICWAPFAQRLM 300
Qy 320 -IYINTESRMMYFQYFNIVALQ---LFYLSASINPILYNLISKYRAAFAFKLLAR-- 373
Db 301 AVYGSTGIESQWFDNFVPSILDYTSGLVYFLSTCINPLLYNIMSKFR-EAPKVTLARHF 359
Qy 374 ----KSRPRGRHRS-----RDTAGEVAGDTGGDTVGYTETSANVTMG 412
Db 360 GLGGKNGRGLPHITYSALRRNTQSGSLRLHT-TDSVRTTWTSMATTTG 406
```

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RESULT 6
S68822
neurotensin receptor 2, levocabastine-sensitive - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C:Accession: S68822
R:Chalon, P.; Vita, N.; Kaghad, M.; Guillemot, M.; Bonnin, J.; Delpach, B.; le Fur, G.;
FBBS Lett. 386, 91-94, 1996
A:Title: Molecular cloning of a levocabastine-sensitive neurotensin binding site.
A:Reference number: S68822; MUID:96228041; PMID:8647296
A:Accession: S68822
A:Molecule type: mRNA
A:Residues: 1-416 <CHA>
A:CROSS-references: UNIPROT:Q63384; GB:X97121; NID:G1483579; PIDN:CAA65787.1; PID:G14835
A:Experimental source: hypothalamus
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:33-58/Domain: transmembrane #status predicted <TM1>
F:70-91/Domain: transmembrane #status predicted <TM2>
F:110-131/Domain: transmembrane #status predicted <TM3>
F:155-175/Domain: transmembrane #status predicted <TM4>
F:204-230/Domain: transmembrane #status predicted <TM5>
F:296-315/Domain: transmembrane #status predicted <TM6>
F:335-361/Domain: transmembrane #status predicted <TM7>

Query Match 18.6%; Score 401; DB 2; Length 416;
Best Local Similarity 29.4%; Pred. No. 1.5e-24;
Matches 122; Conservative 68; Mismatches 145; Indels 80; Gaps 13;

Qy 18 PWPALP-----PCDERCSPPLGALVPVTVAVCLCLFVGVSGNVVTVMLIGRYDRMRT 71
Db 6 PWPPRPSPSAGLSLEARLGVDTRLWAKVLFATALYSLIFAFGTAGNALSVHVVLKARAGRP 65
Qy 72 -TTNLYLGSMAVSDLLILL-GLPDLXR-LWRSRPWVFGPLICRLSLYVGECTVATLLH 128
Db 66 GLRLYHLSLALSALLLVSMPLVNFVWSHPVFGDLGCRGYVFRRLCAVATVLS 125
Qy 129 MTALSVERYLAIICRPLRARVLVTRRRVALIAVLAVALLSAGPFLFVLGV----- 179
Db 126 VASLSAERCLAVCQPLRARRLTTPRTRRLSLVWVASLGLALPMVIMGQKHEVSADG 185
Qy 180 EQDPCISVVPGLNGTARTIA-----SSPLASSPPLMLSRAPPPSPGPETAEEA 228
Db 186 EPEPASRVCTVLVSRATLQVFIOQNVLVSFALPLATLAF-----NGITVNHLM 234
Qy 229 ALFSRECRPSAQLGALRVMLVTTTAYFFLCLSLYGLIGRELWSSRRPLRGPAAAG 288
Db 235 ALYS-QVPSAQAQSSIPSRLLEUSE-----EGLGFTITWRKTLSLGVQASLV 281
Qy 289 RE-----RGHROTQVRLVLLVVLAFIICWLPFHVGRIRIINTED-----SRMMYFQYFNI 338
Db 282 RHKDAQSIRSLQHSQAQLRAIVAVVVICWLPYHARRLMYCVIPDDGWTNELYDFVHYFVM 341
Qy 339 VALQFLYLSASINPILYNLISKYRAAFAFKLLARKSPRGHRSRDTAGEVAGD 393
Db 342 VTNTLFYVSSAVTPILYNAVSSFR---KLFL-----ESLGLSCGE 379

RESULT 7
Jc8011
G protein-coupled neuropeptide pyrokinin-2 receptor (CG8784) - fruit fly (Drosophila mel)
C:Species: Drosophila melanogaster
C>Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C:Accession: Jc8011
R:Rosenkilde, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; DeLotto, I.
Biochem. Biophys. Res. Commun. 309, 485-494, 2003
A:Title: Molecular cloning, functional expression, and gene silencing of two Drosophila
A:Reference number: Jc8011; PMID: 12951076
A:Accession: Jc8011
A:Molecule type: mRNA
A:Residues: 1-658 <ROS>
A:CROSS-references: GB:AY277898
C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as
```

development, diapause, feeding, and behavior.

C;Genetics:

A;Gene: C98784

A;Introns: 160/1; 215/2; 259/3; 326/1; 400/3

C;Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 18.2%; Score 392; DB 2; Length 658;
Best Local Similarity 30.2%; Pred. No. 1.2e-23;
Matches 121; Conservative 55; Mismatches 121; Indels 104; Gaps 15;

QY 1 MGSPPNGSDGEGAREPPWALPPCDERRCSPPFALGVPTAVCLC---LFVGVSGNV 57
DB LGST-NGTNASTMAAD-----SPVDE-----SLTRLALTVCYALIEFVAGVLGNL 126
QY 58 VTVMILGRYDRMTTNLYLGSMAVSDLLIL-GLPFDLYRLWRSRPWFGPLLCLRLSLY 116
DB ITCIVLSRNFWHTATNFYLFNLAVSDLLILVSGIPQELYNLWYDMYPTDAMCIMGSV 186
QY 117 VGEGETYATLLHMTALSVRYLAICRPLARVLVTRRRVRALIAVLMAVALLSAGP--FL 174
DB LGSEMAANATVLTITTAFTVRYTAICHPFHQHTMSKLSRAIKFPAWLAAPTLLALPQAMQ 246
QY 175 FLVGEODGIGSVVGLNGTARIASSPLASSPPLWLSRAPPSGSPGPTABAAALFSRE 234
DB FSV-VYQNEGYCTWENDFYAHV----- 268
QY 235 CRPSPAQLGALRWLVVTTAYFFL--PFLCLSLYLGLIGLELWSSR-----RPLR 282
DB -----FVSGFIFFGPMTAICVLVLGVKLRRLQLSLPRRTFDNR 313
QY 283 GPAAGRGHRGTQVRLVAVVLAFLICWLPFHVGRII-----YINTEDSRMYFSQYF 336
DB GLNAQGR-----VIRMLVAVAVAFPLCWAPFHAQRLMAVYGLNLINIGISRDA-FNDYF 366
QY 337 NIVALQO---LFVLSASINPILNLSKKYRAAFKLLARK 374
DB RILDYTSGLVYFLSTCINPLLYNINSHKFR-EAFKITLTRQ 406

RESULT 8

T15816

hypothetical protein C48C5.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T15816

R;Pavello, A.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of C. elegans cosmid C48C5.

A;Reference number: Z18410

A;Accession: T15816

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-378 <PAV>

A;Cross-references: UNIPROT:Q18701; EMBL:U39994; NID:g1055102; PID:g1055105; PIDN:AAB370

A;Experimental source: strain Bristol N2; clone C48C5

C;Genetics:

A;Gene: CESP:C48C5.1

A;Map position: X

A;Introns: 53/3; 87/2; 136/2; 169/3; 209/3; 231/3; 259/3; 286/1; 327/1

C;Superfamily: adenosine receptor A1

Query Match 17.4%; Score 375; DB 2; Length 378;
Best Local Similarity 28.7%; Pred. No. 1.6e-22;
Matches 97; Conservative 70; Mismatches 135; Indels 36; Gaps 9;

QY 38 LVPVTAVCLCLFVGVSGNVVTVMLIGRYDRMTTNLYLGSMAVSDLLIL-LGLPFDLY 96
DB LYKXTALYIFILVGVIGNTTTCVWKMKHPMMKTHASMYLNLAVSDILVLCVGLPFFVM 110
QY 97 RLWRSRPWFGPLLCLRLSLYGEGETYATLLHMTALSVRYLAICRPL-RAVRLVTRRV 155
DB MNWQYPPFPDPIYCNLKALIAETTSVSIILITLFAERYVAVCHPLFLMKVQPFKNI 170

QY 156 RALIAVLMAVALLSAGPFLFLVGVQDPGIGSVVPLNGTARIASSPLASSPPLMLSRAPP 215
DB GTIIGFTWIFSLCAMP--FAIHRADYIMKSWFGTONRIPVKSCKMC----- 217
QY 216 PSPSPGPTABAAALFSRECRPSPAQLGALRVM-L-VWTTAYFFLFFCLSLYGLIGREL 274
DB -----IAVMF-----EPKLASTPKILFHSAIAFFALPFLFTIVLYARIACKV 260
QY 275 WSSRRLRGPASGRGRHGTQVRLVAVVLAFLICWLPFHVGRIIYINTEDSRMV-YFS 333
DB -SSNRTIQPGELDTEELQMRINALCAVSAFFICYLPFQLQRLLLFPYFDFNEVILTWN 319
QY 334 QYFNVIALQLFYLGSINPILNLSKKYRAAFKLL 371
DB QYMFISGFLFYLATIINPIAYNLASSRFR-RAFKDIL 356

RESULT 9

I57940

somatostatin receptor 5 - rat

N;Alternate names: somatotropin release-inhibiting factor subtype 28 receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

A;Accession: I57940; I57949; S39244

R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.

Mol. Pharmacol. 42, 939-946, 1992

A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref

A;Reference number: I57940; MUID:93125499; PMID:1362243

A;Accession: I57940

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-363 <OCAL>

A;Cross-references: UNIPROT:P30938; GB:L04535; NID:g409238; PIDN:AAAL7029.1; PID:g409239

R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.

Mol. Pharmacol. 44, 1278, 1993

A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref

A;Reference number: I57949; MUID:94088493; PMID:8264565

A;Accession: I57949

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 341-363 <OCA2>

A;Cross-references: GB:S67370; NID:g455947; PIDN:AAB29371.1; PID:g455948

A;Experimental source: pituitary

R;Penetta, R.; Greenwood, M.; Patel, Y.C.

submitted to the EMBL Data Library, August 1993

A;Description: Correction of the nucleotide and amino acid sequence of the rat somatosta

A;Reference number: S39244

A;Accession: S39244

A;Molecule type: mRNA

A;Residues: 309-363 <PEN>

A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912

C;Genetics:

A;Gene: SSTR5

C;Superfamily: vertebrate rhodopsin

Query Match 16.7%; Score 359; DB 2; Length 363;
Best Local Similarity 27.3%; Pred. No. 2.9e-21;
Matches 110; Conservative 60; Mismatches 149; Indels 84; Gaps 12;

QY 5 WNSGDGEGAREPPWALPPCDERRCSPPFLGA---LVPVTAVCLCLFVGVSGNVTVTM 61
DB WNSAASSGNHN--WSLVG-----SASPMGARAVLPVLYLVC--TVGLSGNTLVIY 60
QY 62 LIGRYDRMTTNLYLGSMAVSDLLILGLPFDLYRLWRSRPWFGPLLCLRLSLYVGEBC 121
DB VLVRHAKKTVTVTIINLAVADVFLMGLPFLATQNAVVSWFPGFLCLKLVMLDGIN 120
QY 122 TYATLLHMTALSVRYLAICRPLARVLVTRRRVRALIAVLMAVALLSAGPFLFLVGVEQ 181
DB QFTSIFCLMWSDVRLAVVHPLFSARWRPRVAKMASAAVWVFLSLMLPLLVFADVQE 180
QY 182 DPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSGPTABAAALFSRECRPSPAQ 241

Db 181 G-----WGTCLNS-----W-----PEPVG 194

QY 242 LGALRMLVMTTAYFPFLPCLSLIYGLI-----GRELWSRRRLRGPAAASGRGRHR 294

Db 195 LMGAAFIITVTSVLGFFGPLLVIKLCVLLIWKVKAAGMRVGSRR-----RRRSEP 244

QY 295 QTVRVLLVVVLAFLICWLPFHVGRIIYN-TEDSRMMYFSQYFNIVALQLFYLASINPI 353

Db 245 KVRMMVVVVVLFVGVGCWLPFFIVNVLNLAFTLPEEFTSAGLYFFVVVLS--YANSCANPL 302

QY 354 LYNLISKYRAAFAFKLLARKSRPGFHRSDRTAGEVAGDTGG 396

Db 303 LYGLFSDNFRQSRFKVLCLR-----ROYGMEDADAIEPRDKSG 341

RESULT 10

A46226

somatostatin receptor 3 - human

C:Species: Homo sapiens (man)

C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A46226; S32501

R:Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.; Seino, M.; Endocrinol. 6, 2136-2142, 1992

A:Title: Somatostatin receptors, an expanding gene family: cloning and functional characterization

A:Reference number: A46226; MUID:93149123; PMID:1337145

A:Accession: A46226

A:Molecule type: DNA

A:Residues: 1-418 <YAM>

A:Cross-references: UNIPROT:P32745; GB:M6738; NID:G338498; PID:AAA60592.1; PID:G338499

A:Note: sequence extracted from NCBI backbone (NCBI:123685, NCBIP:123690)

R:Corneish, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent, G.; FEBS Lett. 321, 279-284, 1993

A:Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays preference for D-Trp

A:Reference number: S32501; MUID:93238970; PMID:8097479

A:Accession: S32501

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-418 <COR>

C:Genetics:

A:Gene: GDB:SSTR3

A:Cross-references: GDB:134187; OMIM:182453

A:Map position: 22q13.1-22q13.1

A:Introns: status absent

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F:44-70/Domain: transmembrane #status predicted <TM1>

F:81-106/Domain: transmembrane #status predicted <TM2>

F:118-139/Domain: transmembrane #status predicted <TM3>

F:159-181/Domain: transmembrane #status predicted <TM4>

F:203-233/Domain: transmembrane #status predicted <TM5>

F:255-282/Domain: transmembrane #status predicted <TM6>

F:289-316/Domain: transmembrane #status predicted <TM7>

F:17-30/Binding site: carbonyl/Asn (Asn) (covalent) #status predicted

F:116-191/Disulfide bonds: #status predicted

F:151,251,317,332/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F:251/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted

F:256/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predicted

F:412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 16.6%; Score 357.5; DB 2; Length 418;

Best Local Similarity 26.9%; Pred. No. 4.5e-21;

Matches 101; Conservative 63; Mismatches 146; Indels 65; Gaps 10;

QY 11 PEGAREPPWPAALPPDERRCSFPPL-----GALVPVTAIVCLCLFVVGSGNVVTVMLIGR 65

Db 15 PENA-SSAWPPDATTGNVAGSPAGLAVSGVLIIFVLIIVC--VGLLGNLSLVIVVR 71

QY 66 YRDMRTTNLYLGSMAVSDLLILGLPFDLYLWRSRPVWFGPLLCRLSLYVGECCYAT 125

Db 72 HTAPSPVTNVIYNLALADELFMLGLPF-LAAQNALSYWPFGLMCRVMAVDGINQFTS 130

QY 126 LIHMTALSVERVLAICRPLRARVLTTRRRVRLIAVLNAVALLSAGPFLFLVGVGEQDGI 185

Db 131 IFCLTMSVDRLAVVHPTRSARWRTAPVARTVSAANVWASAVVVLVPPVFSGV----- 184

QY 186 SWFPLNGTARIASSPLASSPPLMLSRAPPSPSPGPETAABAAALFSRECR---PSPAQL 242

Db 185 -----PRGMST-----CHMQWPEPAAA 201

QY 243 GALRMLVMTTAYFPFLPCLSLIYGLIGRELWSRRRLRGPAAASGRGRGHRTQTVRVLLV 302

Db 202 WRAGFIITTAALGFFGPLLVIKLCVLLIWKVKSAGRRVWAPSCQRRRSRRRVTRMVA 261

QY 303 VYLAFLICWLPFHVGRIIYINTE-DSRMMYFSQYFNIVALQLFYLASINPIYLNLSK 361

Db 262 VVALFVLCWMPFYVNLNVNVCPLPEEPAFFGLYFLVVALP--YANSCANPLIYGLFSLYR 319

QY 362 YRAAFAKLLARKSR 376

Db 320 FK-QGFRVRLRPSR 333

RESULT 11

I57955

somatostatin receptor - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I57955

R:Panetta, R.; Greenwood, M.T.; Warszynska, A.; Demchyshyn, L.L.; Day, R.; Niznik, H.B.; Mol. Pharmacol. 45, 417-427, 1994

A:Title: Molecular cloning, functional characterization, and chromosomal localization of the human somatostatin receptor

A:Reference number: I57955; MUID:94195267; PMID:7908405

A:Accession: I57955

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-363 <RES>

A:Cross-references: UNIPROT:P35346; GB:L14865; NID:G431094; PID:AAA20828.1; PID:G431095

C:Genetics:

A:Gene: GDB:SST

A:Cross-references: GDB:119604; OMIM:182450

A:Map position: 3q28-3q28

C:Superfamily: vertebrate rhodopsin

Query Match 16.0%; Score 344; DB 2; Length 363;

Best Local Similarity 27.7%; Pred. No. 4.6e-20;

Matches 106; Conservative 58; Mismatches 131; Indels 88; Gaps 14;

QY 14 AREPPWPAALPP-----CDERR-CSPFP-LGA---LVEPTAVCLCLFVVGSGNVTVML 62

Db 7 ASTFSWNASPGAASGGGDNKTLVGPASAGARAVLVPVLLVC--AAGLGNTLVIVV 64

QY 63 IGRYDRMTTNLYLGSMAVSDLLILGLPFDLYLWRSRPVWFGPLLCRLSLYVGECC 122

Db 65 VLRFAMKKTVTNVIYNLNAVADVLYMLGLPF-LATQNAASFVWPFGLVCLVMTLDGVNQ 123

QY 123 YATLLHMTALSVERVLAICRPLRARVLTTRRRVRLIAVLNAVALLSAGPFLFLVGVGEQD 182

Db 124 FTSVFLTVMSVDRLAVVHPTLSARWRPRAKLASAAVWLSLMSLPLLVFADVOR- 182

QY 183 PGISVVPGLNGTARIASSPLASSPPLMLSRAPPSPSPGPETAABAAALFSRECRSPAQL 242

Db 183 -----GTCNAS-----W-----PEPVCL 196

QY 243 GALRMLVMTTAYFPFLPCLSLIYGLIGRELWSRRRLRGPAAASG-----REGRHQT 296

Db 197 WGAFFIITTAALGFFGPLLVIKLCVLLIWKV-----RAAGRVGCVRRRSRKY 246

QY 297 VRVLLVVAFLICWLPFHVGRIIYI-----NTEDSRMMYFSQYFNIVALQLFYLASIN 351

Db 247 TRMLVVLVVFAGCWLVPFTVNI VNLVALPOEPASAGLYF---FWVI---LSYANSCAN 300

QY 352 PILYNLISKYRAAFAKLLARK 374

Db 301 PVLYGLFSDNFRQSRFKVLCLRK 323

RESULT 12

UN0763
somatostatin receptor 5 - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C/Accession: JN0763
Riyamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A/Title: Cloning, functional expression and pharmacological characterization of a fourth
A/Reference number: JN0762; MUID:93384611; PMID:8373420
A/Accession: JN0763
A/Molecule type: DNA
A/Residues: 1-364 <YAM>
A/Cross-references: UNIPROT:P35346; DDBJ:D16827; NID:G487683; PIDN:BAA04107.1; PID:G48768
C/Comment: This protein is a member of somatostatin receptor family.
C/Genetics:
A/Gene: GDB:SSTR5
A/Cross-references: GDB:138452; OMIM:182455
A/Map position: 16p13.3-16p13.3
A/Introns: #status absent
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; thiol
F/40-66/Domain: transmembrane #status predicted <TM1>
F/77-102/Domain: transmembrane #status predicted <TM2>
F/114-135/Domain: transmembrane #status predicted <TM3>
F/155-177/Domain: transmembrane #status predicted <TM4>
F/196-228/Domain: transmembrane #status predicted <TM5>
F/246-273/Domain: transmembrane #status predicted <TM6>
F/280-307/Domain: transmembrane #status predicted <TM7>
F/13,26,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/112-186/Disulfide bonds: #status predicted
F/242,325/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pr
F/247/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predic
F/320/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 16.0%; Score 344; DB 2; Length 364;

Best Local Similarity 27.7%; Pred. No. 4.7e-20;

Matches 106; Conservative 58; Mismatches 131; Indels 88; Gaps 14;

QY 14 AREPPPALPP-----CDERR-CSPFP-LGA--LVPVTAVCLCLFVVGVSGNVVTML 62

DB 7 ASTPSWASSPGNAGSGGDNRTLVGPAPAGARAVLPVLYLVLC--AAGLGNTLVIYV 64

QY 63 IGRYDRMTTNLYLGSMAVSDLLILGLPFDLYLRMRSPWVFGPFLCLSLYVGEGET 122

DB 65 VLRFAMKTVTIYILNLAADVLYMLGLPF-LATQNAASFPPFGPVLCLVMTLDGVNQ 123

QY 123 YATLLHMTALSVERVLAICRPARVLTTRRRVRLIALVLAVALSAGPFLFVGVBOD 182

DB 124 FTSVCLTVMSVDVLYAVHPVLPSSARWRPRVAKLASAAAWLYSLCMLPLLVFADVQE- 182

QY 183 PGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFRCRPSAQL 242

DB 183 -----GGTCNAS-----W-----PEPVGL 196

QY 243 GALRVMLWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAG-REGRHQT 296

DB 197 WGAVFIIYTVNLGFPAPLVICLCYLLIVKV-----RAAGVRVGVCRRSERKV 246

QY 297 VRVLLVWVLAFLICMLPFGVGHIIYI-----NTDSRMVFSQYFNIVALQLFYLSASIN 351

DB 247 TRMLVVLVVFAGVCLPFFTVNVLNVALPOEPASAGLV---FWVI---LSYANSCAN 300

QY 352 PILYNLISKYRAAFAKLLILARK 374

DB 301 PVLYGFLSDFNQSFQKVLCLRK 323

RESULT 13

AS5259

kappa opioid receptor - guinea pig

N/Alternate names: dynorphin receptor

C/Species: Cavia porcellus (guinea pig)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: A55259

R.Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A.; Watson

Proc. Natl. Acad. Sci. U.S.A. 91, 3779-3783, 1994

A/Title: Primary structure and functional expression of a guinea pig kappa opioid (dynor

A/Reference number: A55259; MUID:94224825; PMID:8170987

A/Accession: A55259

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-380 <XIB>

A/Cross-references: UNIPROT:P41144; GB:U04092; NID:G476106; PIDN:AAAG7171.1; PID:G476107

C/Superfamily: vertebrate rhodopsin

C/Keywords: transmembrane protein

Query Match 15.9%; Score 343.5; DB 2; Length 380;

Best Local Similarity 25.1%; Pred. No. 5.3e-20;

Matches 102; Conservative 74; Mismatches 147; Indels 83; Gaps 12;

QY 2 GSPW-----NGSDGPEGAREPP---WPALPCDERRCSPFPGALVPVTAVCCLCLF 49

DB 26 GSAMLPGWAEPDGNGSAGQDEQLEPAHISPAIP-----VIITAVYSVVF 70

QY 50 VVGSGNVVTVMILGRYKDMRTTNLYLGSMAVSDLLILGLPFDLYLRMRSPWVFGPL 109

DB 71 VVGLVGNLVMFVIIRYTKMTATNIYIFNLADALVTTMPFQ-STVYLMNSWPFQDV 129

QY 110 LCRSLYVGEGETATLLHMTALSVERVLAICRPARVLTTRRRVRLIALVLAVALS 169

DB 130 LCKIVISIDYNNMFTSIFTLTMSVDVRYAVCHVPKALDFRTPLKAKIINTICMLSSSV 189

QY 170 AGPFLFVGVQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEA 229

DB 190 GISAILLGTKVREDVDIIE-----CSLQFPDDDYSWWD----- 223

QY 230 LFSRECRPSAQLGALRVMLWVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAGR 289

DB 224 LFMKIC-----VFVFAFVPIVLIIVCYTILMLRL-KSVRLLSG--SREK 265

QY 290 ERGHRQTVRVLVAVLAFICMLPFGVGHIIYI--NTDSRMVFSQYFNIVALQLFYLS 347

DB 266 DNRURITRLVVLVAVVPIICWTPIHIFILVEALGSTSHSTAALSSYYF---CIALGYTN 322

QY 348 ASINPILYNLISKYRAA-----AFKLLARKSRPRGFHRSRDTA 387

DB 323 SSLNPILYAFLDENFKRCFRDFFCFPIKWMERQSTSRVNTVQDPA 368

RESULT 14

JE0296

thyrotropin releasing hormone receptor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C/Accession: JE0296

R. Itadani, H.; Nakamura, T.; Itoh, J.; Iwaasa, H.; Kanatani, A.; Borkowski, J.; Ihara, M

Biochem. Biophys. Res. Commun. 250, 68-71, 1998

A/Title: Cloning and characterization of a new subtype of thyrotropin-releasing hormone

A/Reference number: JE0296; MUID:98407892; PMID:9735333

A/Accession: JE0296

A/Molecule type: mRNA

A/Residues: 1-352 <ITA>

A/Cross-references: UNIPROT:O88820; DDBJ:AB015645; NID:G3660553; PIDN:BAA33437.1; PID:G3

C/Superfamily: adenosine receptor A1

F/26-48/Domain: transmembrane #status predicted <TM1>

F/58-80/Domain: transmembrane #status predicted <TM2>

F/97-118/Domain: transmembrane #status predicted <TM3>

F/142-165/Domain: transmembrane #status predicted <TM4>

F/188-209/Domain: transmembrane #status predicted <TM5>

F/252-273/Domain: transmembrane #status predicted <TM6>

F/282-304/Domain: transmembrane #status predicted <TM7>

Query Match 15.7%; Score 339; DB 2; Length 352;

Best Local Similarity 28.8%; Pred. No. 1.1e-19;

Matches 108; Conservative 52; Mismatches 109; Indels 106; Gaps 13;

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A;Reference number: A48789; MUID:94052210; PMID:8234341
A;Accession: A48789
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-380 <RES>
A:Cross-references: EMBL:U00442; NID:g403486; PIDN:AAA18261.1; PID:g403487
C:Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

      Query Match          15.7%   Score 339; DB 2; Length 380;
      Best Local Similarity 25.5%; Pred. No. 1.2e-19;
      Matches 103; Conservative 75; Mismatches 146; Indels 80; Gaps 13;

Qy    6  NGSDGPEGAREPP---WPALPPCDERRCSFPPLGALVPVTAVCILCLFWVGSGNVVTML 62
      ||||| : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db    39  NGSVGEDQLEPAHISPAIP-----VIIITAVSVVFVGVGLGNLSLVNFV 83

Qy    63  IGRYDRMTTNYLYLGSMAYSDLLILGLPFDLYRLWRSRPWWFGPLLCLRLSLVYGEGCT 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    84  IIRYTKMKATNIYIFNLADALVTTMTFFQ-SAVYLMMNSWPGDVLCKIVISIDYYNM 142

Qy    123 YATLLHTALTASYRYIAI CRLPLRARVLVTRRRVRVALIAVLWALLSAGPFPLFVGVEOD 182
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    143 FTSIGFTLTMSVDRYIAVCHPVKALDPRTPLKAIIICICIWLASSVGISAIVLGGTKVR 202

Qy    183 PGISVVVPLNGTIARIASSPLASSPFLWSRAPPSPPGPETAAMAAALFSRECPSPAQL 242
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    203 EDYDVIE-----CSLQPPDDEYSWMD-----LFMKIC----- 229

Qy    243 GALRVMLVTTVAFFLPFLCLSLYGLIGRELSSRRPLRGPASGRGRGHROTIVRLVV 302
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    230 -----VVFVAFVIPLIIVCYTLMIURL-KSVRLLSG--SREKORNLRIITKLVLV 278

Qy    303 VILAFLICLPPHFVGRHYIY--NTEDSRMYFYSQYFNIVALQLFYLSASINPILYNLISK 360
      ||||| : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db    279 VVAVFIICTPIIHFILVEALGSTSHSTAVLSSVYF--CIALGYTNSSLNPVIYAFLDE 335

Qy    361 KYRAA-----APKLLARKSRPRGFRHSRDGTAGEVAG--DTGG 396
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    336 NFKRCRDFRCFFPIKRMEROST----NRVANTVDDPASMRDVG 375

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:44:49 ; Search time 742.96 Seconds
(without alignments)
11075.206 Million cell updates/sec

Title: US-09-719-485-4

Perfect score: 1390

Sequence: 1 atgggcgccttcgaacgg.....acgtgaagacgatgggataa 1390

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1390	100.0	1390	3	Aa45404 cDNA enco
2	1161	83.5	1161	4	Aaf83684 Short for
3	1161	83.5	1161	12	Adn11762 Human mot
4	1078	77.6	1239	3	Aa45403 cDNA enco
5	1078	77.6	1239	4	Aaf85449 Nucleotid
6	1078	77.6	1239	4	Aaf83683 Long form
7	1078	77.6	1239	6	Abk90132 DNA enco
8	1078	77.6	1239	8	Abz42842 Human mot
9	1078	77.6	1239	12	Adn11760 Human mot
10	1078	77.6	1239	12	Ado30072 Human GPC
11	1078	77.6	1239	12	Adq37920 Human G-p
12	1078	77.6	1506	4	Aa165989 Human GPR
13	1052	75.7	110000	10	Adg70447 Human ANG
14	1052	75.7	110000	10	Abz79565 CLD8 and
15	1047.2	75.3	2040	3	Aaa46116 Human G p
16	1047.2	75.3	2040	12	Adg86490 Human hGP
17	1047.2	75.3	2040	12	Adp20283 Human GPC
18	1040.8	74.9	2040	12	Adg86512 Human orp
19	1038	74.7	3066	3	Aa45402 Genomic s
20	754.6	54.3	1203	4	Aaf85448 Nucleotid

21	546	39.3	813	4	Aaf85447 Nucleotid
22	501.2	36.1	1179	6	Abq47146 Oligonucl
23	501.2	36.1	1179	6	Abq47147 Oligonucl
24	437.2	31.5	1179	6	Abq47149 Oligonucl
25	437.2	31.5	1179	6	Abq47148 Oligonucl
26	283	20.4	283	2	Aav28290 Galanin r
27	283	20.4	283	2	Aav32651 Galanin r
28	283	20.4	283	2	Aav44930 Galanin r
29	283	20.4	283	6	Abk14060 Rat galan
30	248.2	17.9	1050	3	Aaz61492 cDNA enco
31	234.8	16.9	1063	2	Aat69754 Swine gro
32	234.8	16.9	1063	2	Aat68662 Pig growt
33	233.2	16.8	1029	2	Aat69755 Swine gro
34	233.2	16.8	1029	2	Aat68663 Pig growt
35	231.6	16.7	1095	3	Aaz45993 cDNA enco
36	231.6	16.7	4009	3	Aaz45967 DNA enco
37	230	16.5	1092	12	Ado29027 Mouse nov
38	229	16.5	250	10	Acas5761 Pig signa
39	229	16.5	250	12	Adi55557 Human pol
40	228.8	16.5	870	8	Abz42674 Human gro
41	228.8	16.5	1122	2	Aat68665 Human gro
42	228.4	16.4	1092	4	Aah27800 Rat growt
43	228.4	16.4	3129	2	Aat69759 Rat growt
44	228.4	16.4	3129	2	Aat68667 Rat growt
45	227.8	16.4	1088	2	Aat69756 Human gro

ALIGNMENTS

RESULT 1

AAZ45404

ID AAZ45404 standard; cDNA; 1390 BP.

AC AAZ45404;

DT 27-MAR-2000 (first entry)

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KW growth hormone secretagogue; GHS-R; peptide-antibody complex;
 KW motilin receptor.

OS Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 1..1161

FT /*tag= a
 FT /product= "motilin receptor GPR-388"

XX WO2004033645-A2.

XX PN 22-APR-2004.

XX PF 06-OCT-2003; 2003WO-US031804.

XX PR 07-OCT-2002; 2002US-0416918P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Jaspers SR, Shepard PO, Bishop PD, Kuijper JL, Deisher TA;

XX WPI; 2004-340913/31.

XX DR P-PSDB; ADN11763.

XX Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,
 XX inhibiting signal transduction in a cell expressing a growth hormone
 XX secretagogue receptor, or treating a metabolic disorder.

XX PS Disclosure: Page 96-98; 100pp; English.

XX The present invention relates to the use of a zsig33 peptide for forming
 CC a peptide-antibody complex, purifying a peptide, inhibiting signal
 CC transduction in a cell expressing a growth hormone secretagogue receptor
 CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite
 CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a
 CC mammal, or treating a metabolic disorder. The peptide is useful for
 CC forming a peptide-antibody complex, purifying a peptide, inhibiting
 CC signal transduction in a cell expressing a GHS-R, decreasing fat
 CC deposition in a mammal, suppressing the appetite of a mammal, inhibiting
 CC growth hormone secretion in pituitary cells of a mammal, or treating a
 CC metabolic disorder. The zsig33 polypeptides can be used to study
 CC proliferation or differentiation in stomach, lung, pituitary,
 CC hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,
 CC skeletal muscle or pancreas. They are also useful in delivering
 CC therapeutic agents. Zsig33 polypeptides, agonists and antagonists are
 CC also useful for promoting wound healing. The polypeptides, nucleic acids
 CC and antibodies are useful for diagnosing, treating or preventing
 CC disorders associated with gastric reflux, gastroparesis, modulation of
 CC secretion of pituitary hormones, including growth hormone, Crohn's
 CC disease, metabolic wasting, gastric ulcers, weight management, or
 CC degenerative disease. The present sequence is the human motilin receptor
 CC GPR38B coding sequence shown in the exemplification of the invention.

XX SQ Sequence 1161 BP; 126 A; 436 C; 372 G; 227 T; 0 U; 0 Other;

Query Match 83.5%; Score 1161; DB 12; Length 1161;
 Best Local Similarity 100.0%; Pred. No. 8e-200;
 Matches 1161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCAGCCCTTGAACGCGAGCAGCGCCCGGAGGGGGCGCGGAGCCCGTGGCCC 60
 DB 1 ATGGCAGCCCTTGAACGCGAGCAGCGCCCGGAGGGGGCGCGGAGCCCGTGGCCC 60
 QY 61 GCGCTGCGCCCTTGGCAGAGCGCGCTGCTCGCCCTTTCCCTGGGGCGCTGTGGCG 120
 DB 61 GCGCTGCGCCCTTGGCAGAGCGCGCTGCTCGCCCTTTCCCTGGGGCGCTGTGGCG 120
 QY 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
 DB 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
 QY 181 ATGCTGATGGGGCGGTACCGGGACATGCGGACCAACCACTTGTACTCTGGGCGCATG 240

DB 181 ATGCTGATGGGGCGGTACCGGGACATGCGGACCAACCACTTGTACTCTGGGCGCATG 240
 QY 241 GCGGTGTCGACCTACTCATCTGCTCGGGCTGCGGTTCGACCTGTATCCGCTCTGGGCG 300
 DB 241 GCGGTGTCGACCTACTCATCTGCTCGGGCTGCGGTTCGACCTGTATCCGCTCTGGGCG 300
 QY 301 TCGGGGCGCTGGGTTCGGGCGCTGCTGTGCGGCTGCTCCCTCTAGCTGGGCGAGGCG 360
 DB 301 TCGGGGCGCTGGGTTCGGGCGCTGCTGTGCGGCTGCTCCCTCTAGCTGGGCGAGGCG 360
 QY 361 TGCACCTACGCGACGCTGCTGCACATGACCGCGCTCAGCGTCGAGCGCTACTTGCCCATC 420
 DB 361 TGCACCTACGCGACGCTGCTGCACATGACCGCGCTCAGCGTCGAGCGCTACTTGCCCATC 420
 QY 421 TCGCGCGCTGTCGGGCGCGCTGTTGTATACCGGCGCGCTGTCGGGCGCTATTCGCT 480
 DB 421 TCGCGCGCTGTCGGGCGCGCTGTTGTATACCGGCGCGCTGTCGGGCGCTATTCGCT 480
 QY 481 GTGCTCTGGGCGGTGGGCGCTGCTCTGCGCGTCCCTTCTTGTCTGCTGGGCGTGGAG 540
 DB 481 GTGCTCTGGGCGGTGGGCGCTGCTCTGCGCGTCCCTTCTTGTCTGCTGGGCGTGGAG 540
 QY 541 CAGGACCCCGGCACTCTCCGTAGTCCCGGCGCTCAATGTCACCGCGCGATCGCTCTCTCG 600
 DB 541 CAGGACCCCGGCACTCTCCGTAGTCCCGGCGCTCAATGTCACCGCGCGATCGCTCTCTCG 600
 QY 601 CCTCTGCGCTGTCGGCGCGCTCTGCGTCTGCGGGGCGCCACCGCGCTGTCGGGCGCTG 660
 DB 601 CCTCTGCGCTGTCGGCGCGCTCTGCGTCTGCGGGGCGCCACCGCGCTGTCGGGCGCTG 660
 QY 661 GGGCCGAGACCGCGGAGCGCGCGCTGTTACGCGCGAATGCGCGCGCGAGCCCGCG 720
 DB 661 GGGCCGAGACCGCGGAGCGCGCGCTGTTACGCGCGAATGCGCGCGCGAGCCCGCG 720
 QY 721 CAGCTGGGCGCGCTGCGGTGTCATGCTGGGTGTCACCGCGCTACTTCTTCTGCGCTTT 780
 DB 721 CAGCTGGGCGCGCTGCGGTGTCATGCTGGGTGTCACCGCGCTACTTCTTCTGCGCTTT 780
 QY 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGCTGTGGAGCAGCGGGGCGG 840
 DB 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGCTGTGGAGCAGCGGGGCGG 840
 QY 841 CTGCGAGCCCGCGCGCTCGGGGCGGAGAGGCGCACCGCGAGACCGTCCGCTCTCTG 900
 DB 841 CTGCGAGCCCGCGCGCTCGGGGCGGAGAGGCGCACCGCGAGACCGTCCGCTCTCTG 900
 QY 901 CGTAAGTGGAGCCCGCGGTGTTCCAAAGACGCTGCTGCAGTCCGCGCGCGGGGAGCC 960
 DB 901 CGTAAGTGGAGCCCGCGGTGTTCCAAAGACGCTGCTGCAGTCCGCGCGCGGGGAGCC 960
 QY 961 GCGCAACGCTGGGTTCCTTCCCTGCTGCGCGCGAGCTCTGGGCGCGCTTCCAGCTCCC 1020
 DB 961 GCGCAACGCTGGGTTCCTTCCCTGCTGCGCGCGAGCTCTGGGCGCGCTTCCAGCTCCC 1020
 QY 1021 TTTCCTATTTCGATTCCAGCCTCCACCGCGGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1080
 DB 1021 TTTCCTATTTCGATTCCAGCCTCCACCGCGGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1080
 QY 1081 CTGCTGCGCTTCCAGCGTGGCAGATCATTTATACAAACGAGGATTCGCGGATGAT 1140
 DB 1081 CTGCTGCGCTTCCAGCGTGGCAGATCATTTATACAAACGAGGATTCGCGGATGAT 1140
 QY 1141 GTACTTCTCTCAGTACTTTAA 1161
 DB 1141 GTACTTCTCTCAGTACTTTAA 1161

RESULT 4
 AAZ45403
 ID AAZ45403 standard; cDNA; 1239 BP.
 XX
 AC AAZ45403;

QY 1201 CAACCCATCTCTACACCTCATTTCAAGAAGTACAGAGCGGGGCTTTAAACTGCT 1260
 DB 1050 CAACCCATCTCTACACCTCATTTCAAGAAGTACAGAGCGGGGCTTTAAACTGCT 1109
 QY 1261 GCTGCAAGGAAGTCCAGGCGGAGAGGCTTCCACAGAAACAGGAGCACTGCGGGGGAAGT 1320
 DB 1110 GCTGCAAGGAAGTCCAGGCGGAGAGGCTTCCACAGAAACAGGAGCACTGCGGGGGAAGT 1169
 QY 1321 TGCAGGGGACACTGAGAGAGACACGGTGGGCTACACCGAGACAAGCGCTAACGTGAGAC 1380
 DB 1170 TGCAGGGGACACTGAGAGAGACACGGTGGGCTACACCGAGACAAGCGCTAACGTGAGAC 1229
 QY 1381 GATGGGATAA 1390
 DB 1230 GATGGGATAA 1239

RESULT 5

AAF85449

ID AAF85449 standard; cDNA; 1239 BP.

XX AAF85449;

XX 23-JUL-2001 (first entry)

XX Nucleotide sequence of a human motilin receptor polypeptide.

XX Motilin receptor; gastrointestinal disease; gastric motility disorder;
 KW gastroparesis; irritable bowel syndrome; diarrhoea; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FH 1..1239

FT CDS

FT /*tag= a

FT /note= "motilin receptor"

XX WO200132710-A1.

XX 10-MAY-2001.

XX 25-OCT-2000; 2000WO-US029426.

XX 29-OCT-1999; 99US-0162264P.

XX (MERI) MERCK & CO INC.

XX Tan C, McKee K;

XX WPI; 2001-343479/36.

XX P-PSDB; AAB68478.

XX Novel polypeptides related to dog and rabbit motilin receptor

PT polypeptide, comprising unique regions from dog and motilin receptor

PT amino acid sequence, useful for identifying compounds for treating

PT diarrhea in humans.

XX Disclosure; Page 34; 42pp; English.

XX The present sequence encodes a human motilin receptor polypeptide. The
 CC specification describes a unique sequence present in exon 1 of the dog
 CC motilin receptor, which is not present in human or Sphaeroides nephelus
 CC 75E7 motilin receptor sequences. The unique nucleic acid sequence is
 CC useful for measuring the ability of a compound to affect motilin receptor
 CC activity. Motilin receptor polynucleotides and polypeptides are used to
 CC identify therapeutic compounds which are useful for treating
 CC gastrointestinal diseases and disorders such as gastric motility
 CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea

SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match 77.6%; Score 1078; DB 4; Length 1239;

Best Local Similarity 89.1%; Pred. No. 7e-185;

Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;
 QY 1 ATGGGAGCCCTCTGGAACGCGACGCGCCCGAGGGGCGCGGAGCGCCGCTGGCCCC 60
 DB 1 ATGGGAGCCCTCTGGAACGCGACGCGCCCGAGGGGCGCGGAGCGCCGCTGGCCCC 60
 QY 61 GCGTGCCTGCGCTTTCGACGAGCGCGCTGCTCGCCCTTTCCCTTGGGGGCGCTGGTCCG 120
 DB 61 GCGTGCCTGCGCTTTCGACGAGCGCGCTGCTCGCCCTTTCCCTTGGGGGCGCTGGTCCG 120
 QY 121 GTGACCGCTGTGTCCCTGTCTGCTGCTGGGGTGAAGCGGCAACGTTGACCGGTG 180
 DB 121 GTGACCGCTGTGTCCCTGTCTGCTGCTGGGGTGAAGCGGCAACGTTGACCGGTG 180
 QY 181 ATGCTGATCGGGCGCTACCGGGACATCGGACACCACTTGTACCTTGGGCGAGCATG 240
 DB 181 ATGCTGATCGGGCGCTACCGGGACATCGGAGCACCACTTGTACCTTGGGCGAGCATG 240
 QY 241 GCCGTGTCGACCTTACTCATCTCGGGTGCCTGCTGCACTGTGACCTGTGGCGC 300
 DB 241 GCCGTGTCGACCTTACTCATCTCGGGTGCCTGCTGCACTGTGACCTGTGGCGC 300
 QY 301 TCGCGGCGCTGGGTGTTGGGCGCGCTGCTGCGCGCGCTGCTCTACGTGGGCGAGGGC 360
 DB 301 TCGCGGCGCTGGGTGTTGGGCGCGCTGCTGCGCGCGCTGCTCTACGTGGGCGAGGGC 360
 QY 361 TGCACCTACGCCACGCTGTGCACATGACCGCGCTCAGCGTCGAGCGCTACCTGGCCATC 420
 DB 361 TGCACCTACGCCACGCTGTGCACATGACCGCGCTCAGCGTCGAGCGCTACCTGGCCATC 420
 QY 421 TGGCGCGCGCTCGCGCGCGCGCTTGTGGTCAACCGGCGCGCGCTCGGGCGCTCATCGCT 480
 DB 421 TGGCGCGCGCTCGCGCGCGCGCTTGTGGTCAACCGGCGCGCGCTCGGGCGCTCATCGCT 480
 QY 481 GTGCTCTGGGCGGTGGCGCTGCTCTGCGCGCTCCCTTCTTGTTCCTGGTGGCGTCCAG 540
 DB 481 GTGCTCTGGGCGGTGGCGCTGCTCTGCGCGCTCCCTTCTTGTTCCTGGTGGCGTCCAG 540
 QY 541 CAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGACACCGCGCGGATCGCTCTCTCG 600
 DB 541 CAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGACACCGCGCGGATCGCTCTCTCG 600
 QY 601 CCTCTGGCTCTGTCGCGCGCTCTCTGCGTCTGCGGGGCGGCGCGCGCTCCCGCGCTCG 660
 DB 601 CCTCTGGCTCTGTCGCGCGCTCTCTGCGTCTGCGGGGCGGCGCGCGCTCCCGCGCTCG 660
 QY 661 GGGCGCGAGACCGGGAGCGCGCGCTGTTTACGCGCGGAAATGCGCGCGGAGCGCCCGCG 720
 DB 661 GGGCGCGAGACCGGGAGCGCGCGCTGTTTACGCGCGGAAATGCGCGCGGAGCGCCCGCG 720
 QY 721 CAGCTGGGCGCGCTGCGTGTCAATGCTGTGGGTACACCGCGCTACTTCTTCTGGCCCTTT 780
 DB 721 CAGCTGGGCGCGCTGCGTGTCAATGCTGTGGGTACACCGCGCTACTTCTTCTGGCCCTTT 780
 QY 781 CTGTGCTCAGATCTCTACGGGTCAATCGGGGCGGAGCTGTGAGCAGCGCGCGCGCG 840
 DB 781 CTGTGCTCAGATCTCTACGGGTCAATCGGGGCGGAGCTGTGAGCAGCGCGCGCGCGCG 840
 QY 841 CTGCGAGCGCGCGCGCTCGGGGCGGAGAGAGCGCACCGCGAGACCGTCCGCGTCTCG 900
 DB 841 CTGCGAGCGCGCGCGCTCGGGGCGGAGAGAGCGCACCGCGAGACCGTCCGCGTCTCG 900
 QY 901 CGTAAGTGGAGCGCGCGTGGTTCGTAAGACGCGCTGCTGCACTGCGCGCGCGCGCGGACC 960
 DB 901 C----- 901
 QY 961 GCGCAACCGCTGGGTCCCTTCCCTGCTCGCCAGCTCTGGGCGCGCTTCCAGCTCC 1020
 DB 902 ----- 901
 QY 1021 TTTCCTATTTCGATTCCAGCTCCACCGCGCGCTGGTGGTCTTGGCATTTTAAATTG 1080
 DB 902 -----TGTTGGTGGTCTTGGCATTTTAAATTG 929

QY 1081 CTGTTGTCCTTCCAGTTCAGATCAATTTACATAAACACGGAAGATTTCGCGATGAT 1140
 Db 930 CTGTTGTCCTTCCAGTTCGAGAAATCAATTTACATAAACACGGAAGATTTCGCGATGAT 989
 QY 1141 GTACTTCTCAGTACTTTAATCATGCTCGCTCTGCAACTTTTCTATCTGAGCGCATCTAT 1200
 Db 990 GTACTTCTCAGTACTTTAATCATGCTCGCTCTGCAACTTTTCTATCTGAGCGCATCTAT 1049
 QY 1201 CAACCAATCTCTACAACTCTCAATTTCAAAGAAGTACAGAGCGGGCGCTTTAAACTGCT 1260
 Db 1050 CAACCAATCTCTACAACTCTCAATTTCAAAGAAGTACAGAGCGGGCGCTTTAAACTGCT 1109
 QY 1261 GCTCGCAAGAGTCCAGCGGAGAGGCTTCCACAGAAGCAGGACACTCGCGGGGAAGT 1320
 Db 1110 GCTCGCAAGAGTCCAGCGGAGAGGCTTCCACAGAAGCAGGACACTCGCGGGGAAGT 1169
 QY 1321 TGCAGGGGACACTGGAGGAGACACGGTGGGCTACACCGAGCAAGCGTACGTGAAGAC 1380
 Db 1170 TGCAGGGGACACTGGAGGAGACACGGTGGGCTACACCGAGCAAGCGTGAAGAC 1229
 QY 1381 CATGGGATAA 1390
 Db 1230 CATGGGATAA 1239

RESULT 6

AAF83683
 ID AAF83683 standard; DNA; 1239 BP.

AC AAF83683;

XX 23-JUL-2001 : (first entry)

XX Long form of motilin receptor, GPR-38A isoform encoding DNA.

XX zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R; ds;
 KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38A; isoform.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 1. 1239
 FN /*tag=
 FT /product= "GPR-38A"
 FT

XX WO200138355-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US032074.

XX 22-NOV-1999; 99US-0166765P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

XX WPI; 2001-355879/37.

XX P-PSDB; AAB62652.

XX Forming reversible peptide receptor complex for purifying cell and
 PT peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide.

XX Disclosure; Page 102-104; 111pp; English.

XX The invention relates to a method of forming a reversible peptide-
 CC receptor complex that involves providing an immobilized receptor, and
 CC contacting the receptor with a zsig33 peptide (comprising residues 24-37

CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
 CC is useful for purifying cells, purifying a peptide, stimulating signal
 CC transduction in a cell expressing a receptor. It is also useful for
 CC modulating secretion of hormones, neural development and/or utilization,
 CC gastric contractility, nutrient uptake, secretion of digestive and
 CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal having
 CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the DNA encoding the
 CC long form of motilin receptor, GPR-38A (one of the two isoforms of GPR38
 CC which result from alternative splicing). GPR38 has homology to the human
 CC G-protein coupled receptor, GHS-R

XX SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match 77.6%; Score 1078; DB 4; Length 1239;

Best Local Similarity 89.1%; Pred. No. 7e-185;

Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

QY 1 ATGGGACGCCCTCGAAGCGGACGAGCGGCCCGGAGGGGGCGGAGCCGCCGTGGGCC 60
 Db 1 ATGGGACGCCCTCGAAGCGGACGAGCGGCCCGGAGGGGGCGGAGCCGCCGTGGGCC 60
 QY 61 GCGCTGCGCGCTTTCGAGACGAGCGCGCTGCTCGGCCCTTTTCCCTCGGGGGCGCTGTGCGG 120
 Db 61 GCGCTGCGCGCTTTCGAGACGAGCGCGCTGCTCGGCCCTTTTCCCTCGGGGGCGCTGTGCGG 120
 QY 121 GTGACCGGTGTGTGCTGTGCTTGTCTGCTCGGGGGTACGCGCAACGCTGGTACCGTG 180
 Db 121 GTGACCGGTGTGTGCTGTGCTTGTCTGCTCGGGGGTACGCGCAACGCTGGTACCGTG 180
 QY 181 ATGCTGATCGGGGCTACCGGACATCGGACACCAACCACTTGTACTCGGAGCATG 240
 Db 181 ATGCTGATCGGGGCTACCGGACATCGGACACCAACCACTTGTACTCGGAGCATG 240
 QY 241 GCCGTGTCCGACCTACTATCTCTGCTCGGGGTGCGCTTGCACCTGTACCGCTCTGGCGC 300
 Db 241 GCCGTGTCCGACCTACTATCTCTGCTCGGGGTGCGCTTGCACCTGTACCGCTCTGGCGC 300
 QY 301 TCGGGCGCTGGGTGTTCGGGCGCGCTCTGCGCGCTGTCCTCTAGCTGGGCGAGGCG 360
 Db 301 TCGGGCGCTGGGTGTTCGGGCGCGCTCTGCGCGCTGTCCTCTAGCTGGGCGAGGCG 360
 QY 361 TGCACCTACGCCACGCTGTCACATGACCGCGCTCAGCGCTCAGCGCGTACTGSCCATC 420
 Db 361 TGCACCTACGCCACGCTGTCACATGACCGCGCTCAGCGCTCAGCGCGTACTGSCCATC 420
 QY 421 TCGCGCGCTCTCCGCGCGCGCTTGTGTCAACCGCGCGCGCTCGCGCGCTCATCGCT 480
 Db 421 TCGCGCGCTCTCCGCGCGCGCTTGTGTCAACCGCGCGCGCTCGCGCGCTCATCGCT 480
 QY 481 GTGCTCTGGGCGGTGGCGCTGCTCTCTGCGCGTCCCTTCTTGTCTTGGTGGGCGTCCAG 540
 Db 481 GTGCTCTGGGCGGTGGCGCTGCTCTCTGCGCGTCCCTTCTTGTCTTGGTGGGCGTCCAG 540
 QY 541 CAGGACCCCGGCATCTCCGTAGTCCCGGCTCAATGACCGCGCGCATCGCTCCCTCG 600
 Db 541 CAGGACCCCGGCATCTCCGTAGTCCCGGCTCAATGACCGCGCGCATCGCTCCCTCG 600
 QY 601 CCTCTCGCTCTGTCGCGCGCTCTCTGCGGTCTTCGCGGGCGCCACCGCGCTCCCGCGCTCG 660
 Db 601 CCTCTCGCTCTGTCGCGCGCTCTCTGCGGTCTTCGCGGGCGCCACCGCGCTCCCGCGCTCG 660
 QY 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTACGCGCGCAATGCGGCGCCGAGCCCGCG 720
 Db 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTACGCGCGCAATGCGGCGCCGAGCCCGCG 720


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Qy 421 TCCGCGCCGCTCCGCGCCGCTCTTGTCTACCCGCGCCGCGCTCCGCGCCGCTCATCGCT 480
Db 421 TCCGCGCCGCTCCGCGCCGCTCTTGTCTACCCGCGCCGCGCTCCGCGCCGCTCATCGCT 480
Qy 481 GTGCTCTGGCGCTGGCGCTGCTCTCTCCGCTCCCTTCTTGTCTCTGCTGGCGCTGAG 540
Db 481 GTGCTCTGGCGCTGGCGCTGCTCTCTCCGCTCCCTTCTTGTCTCTGCTGGCGCTGAG 540
Qy 541 CAGGACCCCGCATCTCCGTAAGTCCCGGCTCAATGACACCGCGGATCGCTCTCTCG 600
Db 541 CAGGACCCCGCATCTCCGTAAGTCCCGGCTCAATGACACCGCGGATCGCTCTCTCTCG 600
Qy 601 CCTCTGCTGCTGCGCGCTCTCTGCTCTGCGGCGCCACCGCGCTCCCGCGCTCG 660
Db 601 CCTCTGCTGCTGCGCGCTCTCTGCTCTGCGGCGCCACCGCGCTCCCGCGCTCG 660
Qy 661 GGGCCGAGACCGGGAGCGCGCTGTTACGCGCGAATCGCGCCGAGCCCGCG 720
Db 661 GGGCCGAGACCGGGAGCGCGCTGTTACGCGCGAATCGCGCCGAGCCCGCG 720
Qy 721 CAGCTGGCGCGCTGCTGCTCATGCTGCGGTCAACCGCGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGCGCGCTGCTGCTCATGCTGCGGTCAACCGCGCTACTTCTTCTGCGCTTT 780
Qy 781 CTGTGCTCAGCATCTCTACGCGCTCATCGGCGGAGCTGTGAGCAGCGCGCGCG 840
Db 781 CTGTGCTCAGCATCTCTACGCGCTCATCGGCGGAGCTGTGAGCAGCGCGCGCG 840
Qy 841 CTGGAGCGCGCGCTCCGGCGGAGAGCGCCACCGCGAGCGTCCGCGCTCTG 900
Db 841 CTGGAGCGCGCGCTCCGGCGGAGAGCGCCACCGCGAGCGTCCGCGCTCTG 900
Qy 901 CGTAAGTGGAGCGCGCTGTTCCAAAGACGCTGCTGCAGTCCGCGCCCGCGGAC 960
Db 901 C----- 901
Qy 1021 TTTCTATTTCGATTCAGCTCCACCGCGCTGCTGCTGCTTCTGCGATTTAATTTG 1080
Db 1021 -----TGGTGGTGGTCTTGGCATTTAATTTG 929
Qy 1081 CTGCTTGGCTTCCAGCTTGGAGATCATTTATACAAACAGGAGATTCGCGGATGAT 1140
Db 1081 CTGCTTGGCTTCCAGCTTGGAGATCATTTATACAAACAGGAGATTCGCGGATGAT 989
Qy 1141 GTACTTCTCAGTACTTTAATCATGCTGCTCTGCACTTTTCTATCTGAGCGCATCTAT 1200
Db 1141 GTACTTCTCAGTACTTTAATCATGCTGCTCTGCACTTTTCTATCTGAGCGCATCTAT 1049
Qy 1201 CAACCAATCTCTACACCTCATTTCAAGAGTACAGCGCGGCGCTTTAACTGCT 1260
Db 1201 CAACCAATCTCTACACCTCATTTCAAGAGTACAGCGCGGCGCTTTAACTGCT 1109
Qy 1261 GCTCGAAGGAGTCCAGCGCGAGGCTTCCACAGAGAGGAGACACTGCGGGGAGT 1320
Db 1110 GCTCGAAGGAGTCCAGCGCGAGGCTTCCACAGAGAGGAGACACTGCGGGGAGT 1169
Qy 1321 TGCAGGGGACACTGAGGAGACACGGTGGGTACACCGAGACAGCGCTAACGTGAAGAC 1380
Db 1170 TGCAGGGGACACTGAGGAGACACGGTGGGTACACCGAGACAGCGCTAACGTGAAGAC 1229
Qy 1381 GATGGGATAA 1390
Db 1230 GATGGGATAA 1239
```

RESULT 8

ABZ42842

ID ABZ42842 standard; DNA; 1239 BP.

XX

AC ABZ42842;
XX 04-MAR-2003 (first entry)
XX Human motilin receptor GPR38 nucleotide SEQ ID NO:472.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX Homo sapiens.
OS
XX WO200261087-A2.
XX
XX 08-AUG-2002.
XX
XX 19-DEC-2001; 2001WO-US050107.
XX
XX 19-DEC-2000; 2000US-0257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX Burmer GC, Roush CL, Brown JP;
XX WPI; 2003-046718/04.
XX P-PSDB; ABP81993.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
XX Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match

Best Local Similarity 77.6%; Score 1078; DB 8; Length 1239;

Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

QY 1 ATGGGAGCCCTTGAAAGGAGAGCGGCGCCGAGGGGGCGCGGAGCCCGCCGTGGCCC 60
Db 1 ATGGGAGCCCTTGAAAGGAGAGCGGCGCCGAGGGGGCGCGGAGCCCGCCGTGGCCC 60
QY 61 GCGTGGCCGCTTGCGAGAGCGCGCTGCTCGCCCTTTCCCTTGGGGGCGCTGGTGGCG 120
Db 61 GCGTGGCCGCTTGCGAGAGCGCGCTGCTCGCCCTTTCCCTTGGGGGCGCTGGTGGCG 120
QY 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 ATGCTGATCGGGCGCTACCGGAGCATGCGGACCAACCACTTGTACTCTGGGAGCATG 240
Db 181 ATGCTGATCGGGCGCTACCGGAGCATGCGGACCAACCACTTGTACTCTGGGAGCATG 240
QY 241 GCGTGTCCGACCTACTCATCTGCTCGGGGTGCGCTTGCACCTGTACCGGCTCTGGCGC 300
Db 241 GCGTGTCCGACCTACTCATCTGCTCGGGGTGCGCTTGCACCTGTACCGGCTCTGGCGC 300
QY 301 TCGGGCCCTGGGTGTTGGGGCGCTGCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TCGGGCCCTGGGTGTTGGGGCGCTGCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 TGCACTAGCGACGCTGCTGCATGACCGGCTCAGCGTCGAGCGCTACTTGCCCATC 420
Db 361 TGCACTAGCGACGCTGCTGCATGACCGGCTCAGCGTCGAGCGCTACTTGCCCATC 420
QY 421 TCGCGCCGCTCCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 TCGCGCCGCTCCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 GTGCTGTGGCGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 481 GTGCTGTGGCGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 CAGGACCCCGGATCTCGCTAGTCCGCGCTCAATGACCGCGCGATCGCTTCTCCG 600
Db 541 CAGGACCCCGGATCTCGCTAGTCCGCGCTCAATGACCGCGCGATCGCTTCTCCG 600
QY 601 CCTCTGCGCTCGTCCGCGCTCTCTGCTGCTGCGGGCGCCACCGCGCTCCCGCGCTG 660
Db 601 CCTCTGCGCTCGTCCGCGCTCTCTGCTGCTGCGGGCGCCACCGCGCTCCCGCGCTG 660
QY 661 GGGCGCGAGACCGCGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 GGGCGCGAGACCGCGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 CAGCTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 CAGCTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGCGCGCG 840
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGCGCGCG 840
QY 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCCACCGCAGACCGTCCGCGTCTG 900
Db 841 CTGCGAGCGCGCGCGCTCGGGCGGAGAGAGCGCCACCGCAGACCGTCCGCGTCTG 900
QY 901 CGTAAGTGGAGCGCGCGTGGTTCCAAAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 C----- 901
QY 961 GCGCAACGCTGGGTCCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 902 ----- 901
QY 1021 TTTCCTATTTCGATTCAGCCTCCACCGCGTGGTGGTCTGGCATTTATATTTG 1080
Db 902 -----TGTTGGTGGTCTGGCATTTATATTTG 929

QY 1081 CTGTTGCCCTTCCACGTTGGCAGATCATTTACATAAACACGGAAGATTCGCGATGAT 1140
Db 930 CTGTTGCCCTTCCACGTTGGCAGATCATTTACATAAACACGGAAGATTCGCGATGAT 989
QY 1141 GTACTTCTCAGTACTTTAAACATCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 990 GTACTTCTCAGTACTTTAAACATCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049
QY 1201 CAACCCAACTCTTACAACTCATTTCAAGAGTACAGAGCGCGGCTTTAACTGCT 1260
Db 1050 CAACCCAACTCTTACAACTCATTTCAAGAGTACAGAGCGCGGCTTTAACTGCT 1109
QY 1261 GCTCGAAGGAAGTCCAGGCGGAGAGGCTTCCACAGAAGCAGGACACTGCGGGGAAGT 1320
Db 1110 GCTCGAAGGAAGTCCAGGCGGAGAGGCTTCCACAGAAGCAGGACACTGCGGGGAAGT 1169
QY 1321 TGCAGGGGACACTGAGAGAGACACGTTGGGTACACCGAGACAAGCGCTAACGTGAAGAC 1380
Db 1170 TGCAGGGGACACTGAGAGAGACACGTTGGGTACACCGAGACAAGCGCTAACGTGAAGAC 1229
QY 1381 GATGGGATAA 1390
Db 1230 GATGGGATAA 1239
RESULT 9
ADN11760
ID ADN11760 standard; cDNA; 1239 BP.
XX
AC ADN11760;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human motilin receptor GPR-38A coding sequence.
XX
KW ss; gene; human; zsig33; body weight; body mass; antibody; antagonist;
KW gastrointestinal; antiinflammatory; antiulcer; vulnerary;
KW growth hormone secretagogue; GHS-R; peptide-antibody complex;
KW motilin receptor.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT /*tag= a
FT /product= "motilin receptor GPR38A"
XX
FN WO2004033645-A2.
XX
PD 22-APR-2004.
XX
PF 06-OCT-2003; 2003WO-US031804.
XX
PR 07-OCT-2002; 2002US-0416918P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;
XX
XX WPI; 2004-340913/31.
DR P-PSDB; ADN11761.
XX
XX Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,
XX inhibiting signal transduction in a cell expressing a growth hormone
XX secretagogue receptor, or treating a metabolic disorder.
PS Disclosure; Page 94-95; 100pp; English.
XX
XX The present invention relates to the use of a zsig33 peptide for forming
XX a peptide-antibody complex, purifying a peptide, inhibiting signal
XX transduction in a cell expressing a growth hormone secretagogue receptor
XX (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite
XX of a mammal, inhibiting growth hormone secretion in pituitary cells of a

mammal, or treating a metabolic disorder. The peptide is useful for forming a peptide-antibody complex, purifying a peptide, inhibiting signal transduction in a cell expressing a GHS-R, decreasing fat deposition in a mammal, suppressing the appetite of a mammal, inhibiting growth hormone secretion in pituitary cells of a mammal, or treating a metabolic disorder. The zsig33 polypeptides can be used to study proliferation or differentiation in stomach, lung, pituitary, hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine, skeletal muscle or pancreas. They are also useful in delivering therapeutic agents. Zsig33 polypeptides, agonists and antagonists are also useful for promoting wound healing. The polypeptides, nucleic acids and antibodies are useful for diagnosing, treating or preventing disorders associated with gastric reflux, gastroparesis, modulation of secretion of pituitary hormones, including growth hormone, Cohn's disease, metabolic wasting, gastric ulcers, weight management, or degenerative disease. The present sequence is the human motilin receptor GPR38A coding sequence shown in the exemplification of the invention.

SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match 77.6%; Score 1078; DB 12; Length 1239;
Best Local Similarity 89.1%; Pred. No. 7e-185;
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

Qy 1 ATGGGACGCTTGGAGCGGAGCGCGCCCGGAGGGGGCGGAGCGCCGCTGGGCC 60
Db 1 ATGGGACGCTTGGAGCGGAGCGCGCCCGGAGGGGGCGGAGCGCCGCTGGGCC 60

Qy 61 GCGTGCCGCTTGGAGCGGAGCGCGCTGCTGCGCCCTTCCCTGGGGGGCGTGGTGGC 120
Db 61 GCGTGCCGCTTGGAGCGGAGCGCGCTGCTGCGCCCTTCCCTGGGGGGCGTGGTGGC 120

Qy 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
Db 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180

Qy 181 ATGCTGTATCGGGCGCTACCGGACATGCGGACACACCACTTGTACTTGGGAGCATG 240
Db 181 ATGCTGTATCGGGCGCTACCGGACATGCGGACACCACTTGTACTTGGGAGCATG 240

Qy 241 GCGGTGTCGACCTACTCATCTGCTGGGCTGCGCTTGCACCTGTACCGCTCTGGGCG 300
Db 241 GCGGTGTCGACCTACTCATCTGCTGGGCTGCGCTTGCACCTGTACCGCTCTGGGCG 300

Qy 301 TCGGGCCCTGGGTGTTGGGCGCTGCTCTGCGCCCTGTCCCTCTAGTGGGGAGGGC 360
Db 301 TCGGGCCCTGGGTGTTGGGCGCTGCTCTGCGCCCTGTCCCTCTAGTGGGGAGGGC 360

Qy 361 TGCACCTAGCGACGCTGCTGACATGACCGGCTCAGCGTCTGAGCGCTACCTGGCCATC 420
Db 361 TGCACCTAGCGACGCTGCTGACATGACCGGCTCAGCGTCTGAGCGCTACCTGGCCATC 420

Qy 421 TGGCGCCGCTCCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 TGGCGCCGCTCCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

Qy 481 GTGCTCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 GTGCTCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

Qy 541 CAGGACCCGCGATCTCGTAGTCCGCGGCTCAATGACACCGCGGATCGCTTCCTCG 600
Db 541 CAGGACCCGCGATCTCGTAGTCCGCGGCTCAATGACACCGCGGATCGCTTCCTCG 600

Qy 601 CCTCTGCGCTGCTGCGCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 CCTCTGCGCTGCTGCGCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

Qy 661 GGGCCCGAGACCGCGGAGCGCGGCTGTTTACCGCGGATCGCGCCGAGCCCGCG 720
Db 661 GGGCCCGAGACCGCGGAGCGCGGCTGTTTACCGCGGATCGCGCCGAGCCCGCG 720

Qy 721 CAGTGGGCGCGCTGCTGCTCATGCTGTGGGTTCACACCGGCTACTTCTTCTGCGCCCTT 780

Db 721 CAGTGGGCGCGCTGCTGCTCATGCTGTGGGTACACCGGCTACTTCTTCTGCGCCCTT 780

Qy 781 CTGTGCTCTCAGCATCTCTACGGGCTCATCGGGGGAGCTGTGTGAGCAGCGCGGCGC 840

Db 781 CTGTGCTCTCAGCATCTCTACGGGCTCATCGGGGGAGCTGTGTGAGCAGCGCGGCGC 840

Qy 841 CTGGAGGCGCGCGGCTCTGGGGGGAGAGAGGCGCACCGGAGACCGTTCGCGCTCTG 900

Db 841 CTGGAGGCGCGCGGCTCTGGGGGGAGAGAGGCGCACCGGAGACCGTTCGCGCTCTG 900

Qy 901 CGTAAGTGGAGCGCGGCTTCCAAAGACGCTTCCCTGCTGCTGCGCCGCTTCCAGCTCC 960

Db 901 C----- 901

Qy 961 GCGCAACGCTGGGTTCCTTCCCTGCTGCTGCGCCGCTTCCAGCTCC 1020

Db 902 ----- 901

Qy 1021 TTTCTTATTCGATTTCAGCTCCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080

Db 902 -----TGGTGGTGGTTCCTGCGATTTATAATTG 929

Qy 1081 CTGGTGGCTTCCACGTTGGCAGATCATTTACATAAACACGGAAGATTTCGCGATGAT 1140

Db 930 CTGGTGGCTTCCACGTTGGCAGATCATTTACATAAACACGGAAGATTTCGCGATGAT 989

Qy 1141 GTACTTCTCAGTACTTTAAACATCGTCTGCACTTTTCTATCTGAGCGCATCTAT 1200

Db 990 GTACTTCTCAGTACTTTAAACATCGTCTGCACTTTTCTATCTGAGCGCATCTAT 1049

Qy 1201 CAAACCAATCTCTACAACTCATTTCAAAGAGTACAGAGCGGCGCTTTAAACTGCT 1260

Db 1050 CAAACCAATCTCTACAACTCATTTCAAAGAGTACAGAGCGGCGCTTTAAACTGCT 1109

Qy 1261 GCTCGCAGGAGTCCAGGCGGAGGCTTCCACAGAGCAGGACACTGCGGGGAGT 1320

Db 1110 GCTCGCAGGAGTCCAGGCGGAGGCTTCCACAGAGCAGGACACTGCGGGGAGT 1169

Qy 1321 TGCAGGGGACACTCGAGGAGACAGCGTGGGCTACACCGAGACAGCGCTTAACGTAAGAC 1380

Db 1170 TGCAGGGGACACTCGAGGAGACAGCGTGGGCTACACCGAGACAGCGCTTAACGTAAGAC 1229

Qy 1381 GATCGGATAA 1390

Db 1230 GATCGGATAA 1239

RESULT 10
ADO30072
ID ADO30072 standard; cDNA; 1239 BP.
XX AC ADO30072;
XX DT 29-JUL-2004 (first entry)
XX DE Human GPCR GPR38 polynucleotide, SEQ ID NO:1174.
XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
KW cytosolic; antinflammatory; vasotropic; antianemic; antidiabetic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW viricide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.

Db 1050 CAACCAATCTCTACAACTCTTCAAGAGTACAGAGCGCGCTTTAAACTGCT 1109
Qy 1261 GCTCGCAAGGAAGTCCAGCGGAGAGGCTTCCACAGAGAGGAGACACTCGCGGGGAAGT 1320
Db 1110 GCTCGCAAGGAAGTCCAGCGGAGAGGCTTCCACAGAGAGGAGACACTCGCGGGGAAGT 1169
Qy 1321 TGCAGGGACACTGGAGGAGACACGGTGGGCTTACACCGAGACAAGCGCTAACGTGAAGAC 1380
Db 1170 TGCAGGGACACTGGAGGAGACACGGTGGGCTTACACCGAGACAAGCGCTAACGTGAAGAC 1229
Qy 1381 GATGGATAA 1390
Db 1230 GATGGATAA 1239

RESULT 11

ID ADQ37920 standard, DNA; 1239 BP.

XX AC ADQ37920;

XX DT 23-SEP-2004 (first entry)

XX DE Human G-protein-coupled receptor 38 coding sequence.

XX KW ds; gene; antiparkinsonian; neuroprotective; nootropic; cardiovascular;
KW cardiac; vasotropic; antiarteriosclerotic; nephrotropic; uropathic;
KW urology disease; cardiovascular disease;
KW peripheral nervous system disorder; central nervous system disorder;
KW G-protein-coupled receptor 38; GPR38; Parkinson's disease;
KW multiple sclerosis; dementia; myocardial infarction; ischemic disease;
KW atherosclerosis; renal failure; glomerulopathy; urinary incontinence.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 1..1239

XX FT /*tag= a

XX FT /product= "G-coupled receptor protein 38"

XX PN WO2004057328-A2.

XX PD 08-JUL-2004.

XX PF 11-DEC-2003; 2003WO-EP014052.

XX PR 23-DEC-2002; 2002EP-00028753.

XX PA (FARB) BAYER HEALTHCARE AG.

XX PI Golz S, Brueggemeier U, Summer H;

XX DR WPI; 2004-543310/52.

XX DR P-PSDB; ADQ37921.

XX PT Screening therapeutic agents for use in treatment of urology diseases and
XX PT cardiovascular diseases in a mammal, comprises contacting a test compound
XX PT with G-protein-coupled receptor 38, and detecting binding.

XX PS Disclosure; SEQ ID NO 1; 111pp; English.

XX CC The invention relates to a method of screening (M1) for therapeutic
XX CC agents useful in the treatment of a disease chosen from urology diseases,
XX CC cardiovascular diseases and disorders of the peripheral and central
XX CC nervous system in a mammal, comprises contacting a test compound with a G
XX CC -protein-coupled receptor 38 (GPR38) polypeptide, and detecting binding
XX CC of the test compound to the GPR38 polypeptide. (M1) is useful for
XX CC screening therapeutic agents useful in the treatment of a disease chosen
XX CC from urology diseases, cardiovascular diseases and disorders of the
XX CC peripheral and central nervous system in a mammal, such as Parkinson's
XX CC disease, multiple sclerosis, dementia, cardiovascular disorders such as
XX CC myocardial infarction, ischemic diseases, atherosclerosis, and urological

CC disorders such as acute or chronic renal failure, glomerulopathies, and
CC urinary incontinence. This sequence corresponds to the nucleic acid
CC encoding the human G-protein-coupled receptor 38.

XX SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match 77.6%; Score 1078; DB 12; Length 1239;

Best Local Similarity 89.1%; Pred. No. 7e-185;

Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

Qy 1 ATGGGCAAGCCCTCGAAACGGCAGCAGCGCCCGGAGGGGGCGGAGAGCCCGCTGGGCC 60

Db 1 ATGGGCAAGCCCTCGAAACGGCAGCAGCGCCCGGAGGGGGCGGAGAGCCCGCTGGGCC 60

Qy 61 GCGCTGCCCGCTTTCGACGAGCGCGCTGCTCGCCCTTTCCCTTGGGGGCGCTGGTGGCG 120

Db 61 GCGCTGCCCGCTTTCGACGAGCGCGCTGCTCGCCCTTTCCCTTGGGGGCGCTGGTGGCG 120

Qy 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180

Db 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180

Qy 181 ATGCTGATCGGGCGCTACCGGGACATCGGAGACACCACTTGTACTTGGGAGCATG 240

Db 181 ATGCTGATCGGGCGCTACCGGGACATCGGAGACACCACTTGTACTTGGGAGCATG 240

Qy 241 GCCGTGTCGACCTACTCATCTCTCGGGCTGCCCTTTCGACCTGTACCGCTCTGGCGC 300

Db 241 GCCGTGTCGACCTACTCATCTCTCGGGCTGCCCTTTCGACCTGTACCGCTCTGGCGC 300

Qy 301 TCGGGCCCTCGGGTTCGGGCGCGCTGCTTCGGCGCTGCTTCCTCTAGTGGGAGGCGC 360

Db 301 TCGGGCCCTCGGGTTCGGGCGCGCTGCTTCGGCGCTGCTTCCTCTAGTGGGAGGCGC 360

Qy 361 TGCACCTACGCCAGCTGTGTCACATGACCGCGCTCAGCGTCGAGCGCTACTTGGCCATC 420

Db 361 TGCACCTACGCCAGCTGTGTCACATGACCGCGCTCAGCGTCGAGCGCTACTTGGCCATC 420

Qy 421 TCGCGCCCGCTTCCGCGCGCGCTTGTGTACACCGGGCGCGCTCCGCGCGCTCATCGCT 480

Db 421 TCGCGCCCGCTTCCGCGCGCGCTTGTGTACACCGGGCGCGCTCCGCGCGCTCATCGCT 480

Qy 481 GTGCTCTGGGCGGTGGGCGCTGCTCTCTGCGCGGTCCCTTCTTGTCTGCTGGGCGT 540

Db 481 GTGCTCTGGGCGGTGGGCGCTGCTCTCTGCGCGGTCCCTTCTTGTCTGCTGGGCGT 540

Qy 541 CAGGACCCCGCATCTCGTAGTCCCGGCGCTCAATGSCACCGCGCGATCGCCTCTCG 600

Db 541 CAGGACCCCGCATCTCGTAGTCCCGGCGCTCAATGSCACCGCGCGATCGCCTCTCG 600

Qy 601 CCTCTCGCTCGTCCGCGCGCTCTCTGCGTCTCGGGGCGCCACCGCGCTCCCGCGCTCG 660

Db 601 CCTCTCGCTCGTCCGCGCGCTCTCTGCGTCTCGGGGCGCCACCGCGCTCCCGCGCTCG 660

Qy 661 GGGCCGAGACCGCGGAGGCGCGCGCTGTTTCAGCCCGCGAATGCGCGCGAGCCCGCGG 720

Db 661 GGGCCGAGACCGCGGAGGCGCGCGCTGTTTCAGCCCGCGAATGCGCGCGAGCCCGCGG 720

Qy 721 CAGCTGGGCGGCTGCGGTGCTATGCTGGGTGCTACACCGCGCTACTTCTTCTGCGCTTT 780

Db 721 CAGCTGGGCGGCTGCGGTGCTATGCTGGGTGCTACACCGCGCTACTTCTTCTGCGCTTT 780

Qy 781 CTGTGCTCTACGATCTCTACGGGCTCATCGGGGAGAGTGTGTGAGCAGCGCGCGCGG 840

Db 781 CTGTGCTCTACGATCTCTACGGGCTCATCGGGGAGAGTGTGTGAGCAGCGCGCGCGG 840

Qy 841 CTGCGAGCCCGCGCGCTCTCGGGCGGAGAGAGGCTCACCGGAGACCGTTCGCGTCTG 900

Db 841 CTGCGAGCCCGCGCGCTCTCGGGCGGAGAGAGGCTCACCGGAGACCGTTCGCGTCTG 900

Qy 901 CGTAAGTGGAGCCCGCGGTGGTGTCCAAAGACCGCTTGCCTGTCAGTCCGCGCGCGGACC 960

Db 901 C-----

QY 961 GCGAAACGCTGGTCCCTTCCCTGCTGCGCCAGCTCTGGGCGCGCTCCAGCTCCC 1020
 Db 902 ----- 901
 QY 1021 TTCTCTATTTCGATTCAGCCTCCACCCGCGTGGTGGTCTTGGCAATTTATAATTTG 1080
 Db 902 -----TGGTGGTGGTCTTGGCAATTTATAATTTG 929
 QY 1081 CTGGTTGGCTTCCAGCTTGGCAGAAATCATTTACATAAACAAGGATTCGCGATGAT 1140
 Db 930 CTGGTTGGCTTCCAGCTTGGCAGAAATCATTTACATAAACAAGGATTCGCGATGAT 989
 QY 1141 GTACTTCTCAGTACTTTAAACATCGCTCGCTCTGCAACTTTTCTATCTGAGCGATCTAT 1200
 Db 990 GTACTTCTCAGTACTTTAAACATCGCTCGCTCTGCAACTTTTCTATCTGAGCGATCTAT 1049
 QY 1201 CAACCAATCTCTCAACCTCATTTCAAGAAAGTACAGAGCGCGGCTTTAAACTGCT 1260
 Db 1050 CAACCAATCTCTCAACCTCATTTCAAGAAAGTACAGAGCGCGGCTTTAAACTGCT 1109
 QY 1261 GCTCCAGGAGTCCAGCGCAGAGGCTTCCACAGAAGCAGGACACTGCGGGGAAGT 1320
 Db 1110 GCTCCAGGAGTCCAGCGCAGAGGCTTCCACAGAAGCAGGACACTGCGGGGAAGT 1169
 QY 1321 TGCAGGGACACTGGAGGAGACACGGTGGCTTACACCGAGACAAGCGCTAACGTGAAGAC 1380
 Db 1170 TGCAGGGACACTGGAGGAGACACGGTGGCTTACACCGAGACAAGCGCTAACGTGAAGAC 1229
 QY 1381 GATGGGATAA 1390
 Db 1230 GATGGGATAA 1239

RESULT 12

AAI66989
 ID AAI66989 standard; DNA; 1506 BP.
 XX
 AC AAI66989;
 XX
 DT 30-JAN-2002 (first entry)
 DE Human GPR38 variant GPR38V polypeptide encoding DNA.
 XX
 KW GPR38V; variant; antibacterial; cytostatic; analgesic; antiasthmatic;
 KW anti-Parkinsonian; hypertensive; hypotensive; antidiabetic; osteopathic;
 KW antiallergic; antimigraine; neuroleptic; nootropic; anticonvulsant;
 KW antiulcer; antiemetic; cardiac; vaccine; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 1..1506
 FT /*tag= a
 FT /product= "GPR38V"
 XX
 XX
 PN WO200164836-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006277.
 XX
 PR 01-MAR-2000; 2000US-00516315.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 FI Elshourbagy N, Shabon U;
 XX
 DR WPI; 2001-638956/73.
 DR P-PSDB; AAG65822.
 XX
 PT New human GPR38V polypeptide and polynucleotide, useful for treating e.g.
 bacterial, fungal, protozoal and viral infections, cancers or allergies,

PT as vaccines, and for identifying agonists and antagonists potentially
 XX useful in therapy.

PS Claim 2; Page 26; 32pp; English.

XX This DNA encodes a human GPR38 variant (GPR38V) polypeptide. GPR38V can
 CC be expressed by standard recombinant methodology. The polynucleotides and
 CC polypeptides are used in the treatment of bacterial, fungal, protozoal
 CC and viral infections, infections caused by HIV-1 or HIV-2, pain, cancers,
 CC diabetes, obesity, anorexia, asthma, Parkinson's disease, acute heart
 CC failure, hypertension, urinary retentions, osteoporosis, allergies,
 CC ulcers, migraine, psychotic and neurological disorders, or dyskinesias.
 CC They are also useful for identifying agonists and antagonists that are
 CC potentially useful in therapy, as vaccines to induce immunological
 CC response in a mammal. The polypeptides may also be used as immunogens to
 CC produce antibodies immunospecific for the polypeptides, and to identify
 CC membrane bound or soluble receptors

XX Sequence 1506 BP; 207 A; 534 C; 509 G; 256 T; 0 U; 0 Other;

Query Match 77.6%; Score 1078; DB 4; Length 1506;

Best Local Similarity 89.1%; Pred. No. 7.1e-185;

Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;

QY 1 ATGGGCGAGCCCTCGAAACGGCAGCGAGCGGCCCGGCGGCGCGGCGCGCGCGCGCC 60
 Db 268 ATGGGCGAGCCCTCGAAACGGCAGCGAGCGGCCCGGCGGCGCGGCGCGCGCGCGCC 327
 QY 61 GCGCTGCGCGCTTTCGACGAGCGCGCTGCTGCGCCCTTTCCCTTGGGGGCGCTGGTGGCG 120
 Db 328 GCGCTGCGCGCTTTCGACGAGCGCGCTGCTGCGCCCTTTCCCTTGGGGGCGCTGGTGGCG 387
 QY 121 GTGACCGCTGTGTGCGCTGTGCTGCTGCTGCGGGGTGAGCGGCAACGTGGTGACCGTG 180
 Db 388 GTGACCGCTGTGTGCGCTGTGCTGCTGCTGCGGGGTGAGCGGCAACGTGGTGACCGTG 447
 QY 181 ATGCTGATCGGGCGCTACCGGGACATGCGGACACCAACCACTTGTATCTGGGCGAGCATG 240
 Db 448 ATGCTGATCGGGCGCTACCGGGACATGCGGACACCAACCACTTGTATCTGGGCGAGCATG 507
 QY 241 GCGGTGTCGACCTACTCATCTCTCTCGGGGTGCGGTTCGACCTGTACCGCTCTGGGCGC 300
 Db 508 GCGGTGTCGACCTACTCATCTCTCTCGGGGTGCGGTTCGACCTGTACCGCTCTGGGCGC 567
 QY 301 TCGCGGCGCTGGGTGTTGGGCGCGCTCTCTGCGCGCTGCTCCCTAGTGGGCGAGGGCG 360
 Db 568 TCGCGGCGCTGGGTGTTGGGCGCGCTCTCTGCGCGCTGCTCCCTCTACGTGGGCGAGGGC 627
 QY 361 TGCACTTACGCCACCGCTGTGACATGACCGCGCTCAGCGCTCAGCGCTACTTGGCCATC 420
 Db 628 TGCACTTACGCCACCGCTGTGACATGACCGCGCTCAGCGCTCAGCGCTACTTGGCCATC 687
 QY 421 TGCGCGCGCTTCGCGCGCGCGGTCTTGGTACCGCGCGCGCGGTTCGCGCGCTCATCGCT 480
 Db 688 TGCGCGCGCTTCGCGCGCGCGGTCTTGGTACCGCGCGCGCGGTTCGCGCGCTCATCGCT 747
 QY 481 GTGCTCTGGGCGGTGGCGCTGCTCTCTGCGCGGTCCCTTCTTGTCTGGTGGGCGTGGAG 540
 Db 748 GTGCTCTGGGCGGTGGGCGCTGCTCTCTGCGCGGTCCCTTCTTGTCTGGTGGGCGTGGAG 807
 QY 541 CAGGACCCCGGCATCTCCGTAGTCCCGGGCGCTCAATGGCACCGCGCGGATCGCTCTCTCG 600
 Db 808 CAGGACCCCGGCATCTCCGTAGTCCCGGGCGCTCAATGGCACCGCGCGGATCGCTCTCTCG 867
 QY 601 CCTCTCGCTGTGCGCGCGCTCTCTTGGGTCTCGGGGCGCGACCGCGGTCTCCCGCGGTGCG 660
 Db 868 CCTCTCGCTGTGCGCGCGCTCTCTTGGGTCTCGGGGCGCGACCGCGGTCTCCCGCGGTGCG 927
 QY 661 GGGCGCGAGACCGCGAGGCGCGCGCTGTGTTACGCGCGCAATCCGCGCGAGCCCGCGCG 720
 Db 928 GGGCGCGAGACCGCGAGGCGCGCGCTGTGTTACGCGCGCAATCCGCGCGAGCCCGCGCG 987
 QY 721 CAGTGGGCGCGCTGCGTGTGATGCTGTGGGTACACCGCGCTACTTCTTCTGCGCTTT 780

Db 38196 ATGCTGATCGGCGCTACCGGACATCGGACCAACCAACTTGTACCTGGGCGAGCATG 38255
Qy 241 GCCGTGTCGACCTACTCATCTGCTCGGCTGCGTTCGACCTGTACCGCTCTGGCG 300
Db 38256 GCCGTGTCGACCTACTCATCTGCTCGGCTGCGTTCGACCTGTACCGCTCTGGCG 38315
Qy 301 TCGCGGCGCTGGGTGTCGCGCGCTGCTCTGCGCGCTGCTCCCTCTAGTGGGCGAGGGC 360
Db 38316 TCGCGGCGCTGGGTGTCGCGCGCTGCTCTGCGCGCTGCTCCCTCTAGTGGGCGAGGGC 38375
Qy 361 TGCACCTACGCAACGCTGCTGCACATGACCGCGCTCAGCGTCGAGCGCTACTGGCCATC 420
Db 38376 TGCACCTACGCAACGCTGCTGCACATGACCGCGCTCAGCGTCGAGCGCTACTGGCCATC 38435
Qy 421 TGCAGCGCGCTCGGCGCGGCTGCTGCTGCTACCGCGCGCGCTCCGCGCGCTCATCGCT 480
Db 38436 TGCAGCGCGCTCGGCGCGGCTGCTGCTGCTACCGCGCGCGCTCCGCGCGCTCATCGCT 38495
Qy 481 GTGCTCTGGGCGCTGGCGCTGCTCTGCTCGCGCTGCTCTGCTGCTGGGCGCTCGAG 540
Db 38496 GTGCTCTGGGCGCTGGCGCTGCTCTGCTCGCGCTGCTCTGCTGCTGGGCGCTCGAG 38555
Qy 541 CAGGACCCCGGCTATCTCGTAGTCCGCGCTCAATGGACCGCGCGATCGCTCTCTCG 600
Db 38556 CAGGACCCCGGCTATCTCGTAGTCCGCGCTCAATGGACCGCGCGATCGCTCTCTCG 38615
Qy 601 CCTCTCGCTGCTGCGCGCTGCTGCTGCTGCTGCGCGCGCGCTCCGCGCGCTCG 660
Db 38616 CCTCTCGCTGCTGCGCGCTGCTGCTGCTGCTGCGCGCGCGCTCCGCGCGCTCG 38675
Qy 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTTGAGCGCGAATGCGGCGCGAGCCCGCG 720
Db 38676 GGGCCCGAGACCGCGGAGCGCGCGCTGTTGAGCGCGAATGCGGCGCGAGCCCGCG 38735
Qy 721 CAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 38736 CAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38795
Qy 781 CTGTCCTCAGCATCTCTACGGCTCATCGGCGGAGCTGTGAGAGCGCGCGCGCG 840
Db 38796 CTGTCCTCAGCATCTCTACGGCTCATCGGCGGAGCTGTGAGAGCGCGCGCGCG 38855
Qy 841 CTGCGAGGCGCGCGCTCGGCGGAGAGAGCGCCACCGGAGACCGTTCGCGTCTCTG 900
Db 38856 CTGCGAGGCGCGCGCTCGGCGGAGAGAGCGCCACCGGAGACCGTTCGCGTCTCTG 38915
Qy 901 CCGTAGTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 38916 CCGTAGTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38975
Qy 961 GCGCAACGCTGGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 38976 GCGCAACGCTGGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39035
Qy 1021 TTTCTATTTCGATTCCAGCTCCACCGCGCG 1052
Db 39036 TTTCTATTTCGATTCCAGCTCCACCGCGCG 39067

RESULT 14
ABZ79565.0
WP Sequence split into 5 fragments LOCUS ABZ79565 Accession ABZ79565
WP Fragment Name Begin End
WP ABZ79565.0 1 110000
WP ABZ79565.1 100001 210000
WP ABZ79565.2 200001 310000
WP ABZ79565.3 300001 410000
WP ABZ79565.4 400001 410846
ID ABZ79565 standard; DNA; 410846 BP.

XX ABZ79565;

XX 01-JUL-2003 (first entry)

XX CLLD8 and NY-REN-34 encoding DNA.
DE
XX Cytostatic; gene therapy; B-cell chronic lymphocytic leukaemia; BCLL;
KW CLLD8; NY-REN-34; gene; db.
XX Unidentified.
OS
XX Key Location/Qualifiers
FH CDS 294727..309803
FT /*tag= a
FT /product= "CLLD8"
FT 313649..346509
FT /*tag= b
FT /product= "NY-REN-34"
XX
XX WO2003000296-A2.
XX
XX 03-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-GB002857.
XX
XX 21-JUN-2001; 2001GB-00015211.
XX
XX (ISIS-) ISIS INNOVATIONS LTD.
XX
XX Zhang Y, Moffatt M, Cookson W;
PI
XX WPI; 2003-221370/21.
XX
XX Treating B-cell chronic lymphocytic leukemia in an individual by
PT modulating the expression of the CLLD8 and/or the NY-REN-34 gene.
PT
XX Disclosure; Fig 1; 154pp; English.
XX
XX The invention relates to a method for treating B-cell chronic lymphocytic
CC leukaemia (BCLL), comprising modulating the expression of the CLLD8
CC and/or the NY-REN-34 gene. The polynucleotide sequence or gene product of
CC the CLLD8 and/or NY-REN-34 gene or agent is useful for the manufacture of
CC a diagnosis and treatment of BCLL. The current sequence represents CLLD8
CC and NY-REN-34 encoding DNA
XX
SQ Sequence 410846 BP; 125177 A; 83172 C; 81704 G; 120793 T; 0 U; 0 Other;
Query Match 75.7%; Score 1052; DB 10; Length 110000;
Best Local Similarity 100.0%; Pred. No. 4.3e-180;
Matches 1052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGGACCCCTCGAACCGGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
Db 38016 ATGGGACCCCTCGAACCGGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 38075
Qy 61 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGCTTTCCTTGGGGCGCTGCTGCGCG 120
Db 38076 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGCTTTCCTTGGGGCGCTGCTGCGCG 38135
Qy 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 38136 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 38195
Qy 181 ATGCTGATCGGGCGCTACCGGACATGCGGACCAACCACTTGTACCTGGGCGAGCATG 240
Db 38196 ATGCTGATCGGGCGCTACCGGACATGCGGACCAACCACTTGTACCTGGGCGAGCATG 38255
Qy 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGGTTTCGACCTGTACCGCTCTGGGCG 300
Db 38256 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGGTTTCGACCTGTACCGCTCTGGGCG 38315
Qy 301 TCGCGGCGCTGGGTGTCGCGCGCTGCTCTGCGCGCTGCTCCCTCTAGTGGGCGAGGGC 360
Db 38316 TCGCGGCGCTGGGTGTCGCGCGCTGCTCTGCGCGCTGCTCCCTCTAGTGGGCGAGGGC 38375
Qy 361 TGCACCTACGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

Db 38376 TGCACCTAGCCACAGCTGTGCACATGACCGGCTCAGCGTCGAGCGTACCTGCGCATC 38435
Qy 421 TGCCGCCCGCTCCGCGCCCGCTCTGTGTACCCCGGCGCGGTCCGCGCGCTCATCGCT 480
Db 38436 TGCCGCCCGCTCCGCGCCCGCTCTGTGTACCCCGGCGCGGTCCGCGCGCTCATCGCT 38495
Qy 481 GTGCTCTGGCGCGTGGCGCTGTCTCTGCGCGGTCCCTTCTTGTCTCTGTTGGGCGTCAAG 540
Db 38496 GTGCTCTGGCGCGTGGCGCTGTCTCTGCGCGGTCCCTTCTTGTCTCTGTTGGGCGTCAAG 38555
Qy 541 CAGGACCCCGCATCTCCGTAGTCCCGGCGCTCAATGACCGCGCGATGCGCTCTCTCG 600
Db 38556 CAGGACCCCGCATCTCCGTAGTCCCGGCGCTCAATGACCGCGCGATGCGCTCTCTCG 38615
Qy 601 CCTCTGCGCTCTGCGCGCTCTCTGCGGTCTGCGCGGCGCAACCGCGTCCCGCGCTCG 660
Db 38616 CCTCTGCGCTCTGCGCGCTCTCTGCGGTCTGCGCGGCGCAACCGCGTCCCGCGCTCG 38675
Qy 661 GGGCCCGAGACCGCGAGCGCGCGCTGTTTACGCGCGAATGCGCGCGAGCGCCGCG 720
Db 38676 GGGCCCGAGACCGCGAGCGCGCGCTGTTTACGCGCGAATGCGCGCGAGCGCCGCG 38735
Qy 721 CAGCTGGCGCGCTCGGTGTATGCTGTGGTCAACCGCGTACTTCTTCTGCGCTTT 780
Db 38736 CAGCTGGCGCGCTCGGTGTATGCTGTGGTCAACCGCGTACTTCTTCTGCGCTTT 38795
Qy 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGCTGTGAGCAGCGCGCGCG 840
Db 38796 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGCTGTGAGCAGCGCGCGCG 38855
Qy 841 CTGCGAGCCCGCGCTCTGCGGCGGAGAGCGCAACCGCGAGCGTCCGCTCTCTG 900
Db 38856 CTGCGAGCCCGCGCTCTGCGGCGGAGAGCGCAACCGCGAGCGTCCGCTCTCTG 38915
Qy 901 CGTAAGTGAGCGCGCGTGTTCAAAGACGCTGCTGAGTCCGCGCGCGCGCGGAC 960
Db 38916 CGTAAGTGAGCGCGCGTGTTCAAAGACGCTGCTGAGTCCGCGCGCGCGCGGAC 38975
Qy 961 GCGCAACGCTGGGTCCCTTCCCTGCTGCGCGAGCTGTGGGCGCGCTCCAGCTCC 1020
Db 38976 GCGCAACGCTGGGTCCCTTCCCTGCTGCGCGAGCTGTGGGCGCGCTCCAGCTCC 39035
Qy 1021 TTTCTATTTCGATTCAGCTCCACCGCG 1052
Db 39036 TTTCTATTTCGATTCAGCTCCACCGCG 39067

RESULT 15

AAA46116
ID AAA46116 standard; cDNA; 2040 BP.
XX AC AAA46116;
XX DT 22-AUG-2000 (first entry)
XX DE Human G protein coupled receptor hGPR38 (V297K) cDNA SEQ ID NO:129.
XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;
KW ss.
XX OS Homo sapiens.
OS Synthetic.
XX PN WO200022131-A2.
XX PD 20-APR-2000.
XX PF 13-OCT-1999; 99WO-US024065.
XX PR 13-OCT-1998; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.

PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123945P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-0141448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.
XX (AREN-) ARENA PHARM INC.

Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;

Gore M, Liaw CW, Lin I, Lowitz K, White C;

WPI; 2000-317986/27.

P-PSDB; AAB02854.

Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents.

Example 2; Page 166-168; 187pp; English.

The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention

Sequence 2040 BP; 350 A; 630 C; 597 G; 463 T; 0 U; 0 Other;

Query Match 75.3%; Score 1047.2; DB 3; Length 2040;
Best Local Similarity 99.7%; Pred. No. 2.5e-179;
Matches 1049; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ATGGGACGCCCTCGAAACGGCAGCAGCGCCCCGAGGGGGCGCGGAGCCCGTGGGCC 60
Db 1 ATGGGACGCCCTCGAAACGGCAGCAGCGCCCCGAGGGGGCGCGGAGCCCGTGGGCC 60
Qy 61 GCGCTGCGCGCTTGGGACGAGCGCGCTGCTGCGCCCTTCCCTGGGGCGCTGGTGGCG 120
Db 61 GCGCTGCGCGCTTGGGACGAGCGCGCTGCTGCGCCCTTCCCTGGGGCGCTGGTGGCG 120
Qy 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
Db 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
Qy 181 ATGCTGATCGGGCGCTACCGGGACATGCGGGACACACACCACTTGTACCTGGGCAGCATG 240


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Db 181 ATGCTGATCGGCGCTACCGGAGCATCGGACCACTTGTTACTTGGGAGCATG 240
Qy 241 GCGGTGTCGAGCACTACTCTGCTCGGGCTGCGGTTCGACCTGTACCGCTCTGGGCG 300
Db 241 GCGGTGTCGAGCACTACTCTGCTCGGGCTGCGGTTCGACCTGTACCGCTCTGGGCG 300
Qy 301 TCGGGCCCTGGGTGTTTCGGGCGGCTGCTTCGCGCCCTGTCCTTACGTGGGGAGGGC 360
Db 301 TCGGGCCCTGGGTGTTTCGGGCGGCTGCTTCGCGCCCTGTCCTTACGTGGGGAGGGC 360
Qy 361 TGCACCTAGCCACACGCTGCTGCACATGACCGGCTCAGCGTCGAGCGCTACTTGGCCATC 420
Db 361 TGCACCTAGCCACACGCTGCTGCACATGACCGGCTCAGCGTCGAGCGCTACTTGGCCATC 420
Qy 421 TCGCGCCCGCTTCGGCGCGGCTCTTGTGTACCGGCGCGGCTCGCGGCTCATCGCT 480
Db 421 TCGCGCCCGCTTCGGCGCGGCTCTTGTGTACCGGCGCGGCTCGCGGCTCATCGCT 480
Qy 481 GTGCTCTGGGCGGTGGCGGCTGCTCTCGCGCTCCCTTCTTGTTCCTGGTGGGGTCGAG 540
Db 481 GTGCTCTGGGCGGTGGCGGCTGCTCTCGCGCTCCCTTCTTGTTCCTGGTGGGGTCGAG 540
Qy 541 CAGGACCCCGGCATCTCGTATGCCGGGCTCAATGGCACCGCGCGGATCGCTTCCTCG 600
Db 541 CAGGACCCCGGCATCTCGTATGCCGGGCTCAATGGCACCGCGCGGATCGCTTCCTCG 600
Qy 601 CCTCTCGGCTGTGCGCGGCTCTCTGGGCTCTCGCGGCGGCGGCGGCTCGCGGCTCG 660
Db 601 CCTCTCGGCTGTGCGCGGCTCTCTGGGCTCTCGCGGCGGCGGCGGCTCGCGGCTCG 660
Qy 661 GGGCCCGAGACCGCGGAGCGCGGCTGTTTACCGCGGAATGCCGCGGAGCGCGCGCG 720
Db 661 GGGCCCGAGACCGCGGAGCGCGGCTGTTTACCGCGGAATGCCGCGGAGCGCGCGCG 720
Qy 721 CAGCTGGGCGGCTGCTGTCATGCTGGGTACACCGGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGGCGGCTGCTGTCATGCTGGGTACACCGGCTACTTCTTCTGCGCTTT 780
Qy 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGGCGCG 840
Db 781 CTGTGCTCAGCATCCTCTACGGGCTCATCGGGCGGAGCTGTGGAGCAGCGCGGCGCG 840
Qy 841 CTGGAGGCGCGCGGCTCGGGCGGAGAGAGCCACCGGAGAGAGCTCGCGCTCCTG 900
Db 841 CTGGAGGCGCGCGGCTCGGGCGGAGAGAGCCACCGGAGAGAGCTCGCGCTCCTG 900
Qy 901 CGTAAAGTGAGCGCGGCTGTTCCAAAGACGCTGCTGAGTCCGCGCGCGCGGGGACC 960
Db 901 CGTAAAGTGAGCGCGGCTGTTCCAAAGACGCTGCTGAGTCCGCGCGCGCGGGGACC 960
Qy 961 GCGCAACGCTGGTCCCTCCCTGCTCGCGGAGCTGTGGCGCGGCTTCCAGTCCC 1020
Db 961 GCGCAACGCTGGTCCCTCCCTGCTCGCGGAGCTGTGGCGCGGCTTCCAGTCCC 1020
Qy 1021 TTTCTATTTCGATCCAGCTCCACCGCGG 1052
Db 1021 TTTCTATTTCGATCCAGCTCCACCGCGG 1052
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Search completed: April 10, 2005, 23:50:42
Job time : 755.96 secs

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OM nucleic - nucleic search, using sw model

Run on: April 10, 2005, 22:51:55 ; Search time 228.453 Seconds
(without alignments)
9955.765 Million cell updates/sec

Title: US-09-719-485-4
Perfect score: 1390
Sequence: 1 atgggcagccctggaacgg.....acgtgaagacatgggataa 1390

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	20.4	283	3	US-08-993-088A-4
2	283	20.4	283	3	US-08-993-424B-4
3	283	20.4	283	4	US-09-603-680-4
4	248.2	17.9	1050	4	US-09-762-661A-1
5	234.8	16.9	1063	3	US-09-077-675A-1
6	234.8	16.9	1063	4	US-09-077-674-1
7	231.6	16.7	1095	4	US-09-743-475-2
8	231.6	16.7	4009	4	US-09-743-475-1
9	230	16.5	1029	3	US-09-077-675A-4
10	230	16.5	1029	4	US-09-077-674-4
11	229	16.5	250	4	US-09-016-434-359
12	228.8	16.5	1122	3	US-09-077-675A-9
13	228.8	16.5	1122	4	US-09-077-674-9
14	228.4	16.4	1092	3	US-09-077-675A-15
15	228.4	16.4	1092	4	US-09-077-674-15
16	228.4	16.4	3129	3	US-09-077-675A-14
17	228.4	16.4	3129	4	US-09-077-674-14
18	227.8	16.4	1088	3	US-09-077-675A-6
19	227.8	16.4	1088	4	US-09-077-674-6
20	227.8	16.4	1101	4	US-09-016-434-1148
21	227.8	16.4	1101	4	US-09-170-496D-87
22	227.8	16.4	1101	4	US-09-170-496D-209
23	227.8	16.4	1101	4	US-09-364-425B-44
24	153	11.0	836	3	US-09-077-675A-11
25	153	11.0	836	4	US-09-077-674-11
26	134.8	9.7	729	4	US-09-684-725-1
27	134.8	9.7	1239	4	US-09-949-016-4230

28	134.8	9.7	1248	3	US-09-545-944-1
29	134.8	9.7	1360	4	US-09-341-016A-2
30	134.8	9.7	16914	4	US-09-949-016-15972
31	127	9.1	1233	4	US-09-826-509-536
32	127	9.1	1575	3	US-08-858-876A-1
33	127	9.1	1575	3	US-09-472-880-1
34	125.4	9.0	1342	3	US-08-832-399-1
35	125.4	9.0	1342	3	US-09-372-498-1
36	123	8.8	1257	4	US-09-826-509-534
37	123	8.8	4080	4	US-09-016-434-1346
38	122.2	8.8	1529	3	US-08-858-876A-3
39	122.2	8.8	1529	3	US-09-472-880-3
40	122	8.8	1095	4	US-09-826-509-576
41	122	8.8	1285	4	US-09-016-434-1366
42	120	8.6	1535	3	US-09-668-680-12
43	119	8.6	1212	4	US-09-170-496D-113
44	119	8.6	1212	4	US-09-170-496D-223
45	119	8.6	1212	4	US-09-743-742B-3

ALIGNMENTS

RESULT 1
US-08-993-088A-4
; Sequence 4, Application US/08993088A
; Patent No. 6287855
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Sullivan, Kathleen
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
; NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P. O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,088A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...283
; OTHER INFORMATION: cdna probe
US-08-993-088A-4

Sequence 1, Appli
Sequence 2, Appli
Sequence 15972, A
Sequence 536, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 534, App
Sequence 1346, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 576, App
Sequence 1366, App
Sequence 12, Appli
Sequence 113, App
Sequence 223, App
Sequence 3, Appli

Query Match 20.4%; Score 283; DB 3; Length 283;
 Best Local Similarity 100.0%; Pred. No. 2.2e-50;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 TCGGACACCAACCTGTACCTGGGAGCATGGCGGTGCGACCTACTCATCTCTGC 265
 Db 1 TCGGACACCAACCTGTACCTGGGAGCATGGCGGTGCGACCTACTCATCTCTGC 60

QY 266 TCGGCTCGCGCTCGACCTGTACCGCTCTGGCGCTCGGCGCTTGGGTGTTGGGCGGC 325
 Db 61 TCGGCTCGCGCTCGACCTGTACCGCTCTGGCGCTCGGCGCTTGGGTGTTGGGCGGC 120

QY 326 TGCTCTCGCGCTCGACCTGTACCGCTCTGGCGCTCGGCGCTTGGGTGTTGGGCGGC 385
 Db 121 TGCTCTCGCGCTCGACCTGTACCGCTCTGGCGCTCGGCGCTTGGGTGTTGGGCGGC 180

QY 386 TGACCGCGCTCAGCTCGAGCGCTACCTGGGCGGTGACCTACGCCACGCTGTGTCACA 445
 Db 181 TGACCGCGCTCAGCTCGAGCGCTACCTGGGCGGTGACCTACGCCACGCTGTGTCACA 240

QY 446 TGGTCACCGCGCGCGCTCGGCGCTCATCGCTGTGCTCTG 488
 Db 241 TGGTCACCGCGCGCGCTCGGCGCTCATCGCTGTGCTCTG 283

RESULT 2

US-08-993-424B-4
 ; Sequence 4, Application US/08993424B
 ; Patent No. 6337206
 ; GENERAL INFORMATION:
 ; APPLICANT: Tan, Carina
 ; TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALR2 AND
 ; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merck & Co., Inc.
 ; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
 ; CITY: Rahway
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07065-0900
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/993,424B
 ; FILING DATE: 18-DEC-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/033,851
 ; FILING DATE: 27-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heber, Sheldon O.
 ; REGISTRATION NUMBER: 38,179
 ; REFERENCE/DOCKET NUMBER: 19846NP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 732-594-1958
 ; TELEFAX: 732-594-4720
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 283 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Other
 ; FEATURE:
 ; NAME/KEY: Other
 ; LOCATION: 1...283
 ; OTHER INFORMATION: cdna probe

US-08-993-424B-4

Query Match 20.4%; Score 283; DB 3; Length 283;
 Best Local Similarity 100.0%; Pred. No. 2.2e-50;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 TCGGACACCAACCTGTACCTGGGAGCATGGCGGTGCGACCTACTCATCTCTGC 265
 Db 1 TCGGACACCAACCTGTACCTGGGAGCATGGCGGTGCGACCTACTCATCTCTGC 60

QY 266 TCGGCTCGCGCTCGACCTGTACCGCTCTGGCGCTCGGCGCTTGGGTGTTGGGCGGC 325
 Db 61 TCGGCTCGCGCTCGACCTGTACCGCTCTGGCGCTCGGCGCTTGGGTGTTGGGCGGC 120

QY 326 TGCTCTCGCGCTCGACCTGTACCGCTCTGGCGCTCGGCGCTTGGGTGTTGGGCGGC 385
 Db 121 TGCTCTCGCGCTCGACCTGTACCGCTCTGGCGCTCGGCGCTTGGGTGTTGGGCGGC 180

QY 386 TGACCGCGCTCAGCTCGAGCGCTACCTGGGCGGTGACCTACGCCACGCTGTGTCACA 445
 Db 181 TGACCGCGCTCAGCTCGAGCGCTACCTGGGCGGTGACCTACGCCACGCTGTGTCACA 240

QY 446 TGGTCACCGCGCGCGCTCGGCGCTCATCGCTGTGCTCTG 488
 Db 241 TGGTCACCGCGCGCGCTCGGCGCTCATCGCTGTGCTCTG 283

RESULT 3

US-09-603-680-4
 ; Sequence 4, Application US/09603680
 ; Patent No. 6544753
 ; GENERAL INFORMATION:
 ; APPLICANT: Tan, Carina
 ; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
 ; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merck & Co., Inc.
 ; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
 ; CITY: Rahway
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07065-0900
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/603,680
 ; FILING DATE: 26-Jun-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/033,851
 ; FILING DATE: 27-DEC-1996
 ; APPLICATION NUMBER: 08/993,088
 ; FILING DATE: 18-DEC-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heber, Sheldon O.
 ; REGISTRATION NUMBER: 38,179
 ; REFERENCE/DOCKET NUMBER: 19846 CA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 732-594-1958
 ; TELEFAX: 732-594-4720
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 283 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Other

FEATURE:
NAME/KEY: Other
LOCATION: 1...283
OTHER INFORMATION: cDNA probe
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-603-680-4

Query Match 20.4%; Score 283; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.2e-50;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 TCGGACGACCAACAACTTGTACCTGGGAGCATGGCGGTGTCGACCTACTCATCTCTGCG 265
Db 1 TCGGACGACCAACAACTTGTACCTGGGAGCATGGCGGTGTCGACCTACTCATCTCTGCG 60

Qy 266 TCGGCTGCGGTTCGACCTGTACCGCTCTGCGCTCGCGGCTTGGGTGTTTCGGGCGCG 325
Db 61 TCGGCTGCGGTTCGACCTGTACCGCTCTGCGCTCGCGGCTTGGGTGTTTCGGGCGCG 120

Qy 326 TGCTTGGCGCTGTCCTCTACGTGGGAGGCTGCACTACGCCAGCTGCTGCA 385
Db 121 TGCTTGGCGCTGTCCTCTACGTGGGAGGCTGCACTACGCCAGCTGCTGCA 180

Qy 386 TGACCGCTCAGCTGCGAGCTACCTGGCCATCTGGCGGCTCGCGGCTCGCGGCTCGCT 445
Db 181 TGACCGCTCAGCTGCGAGCTACCTGGCCATCTGGCGGCTCGCGGCTCGCGGCTCGCT 240

Qy 446 TGGTCACCGCGCGCGCTCGCGGCTCATCGCTGCTGTG 488
Db 241 TGGTCACCGCGCGCGCTCGCGGCTCATCGCTGCTGTG 283

RESULT 4

US-09-762-661A-1
; Sequence 1, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Palyha, Oksana C.
; APPLICANT: Smith, Roy G.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1050)
; OTHER INFORMATION: n = A,T,C or G
US-09-762-661A-1

Query Match 17.9%; Score 248.2; DB 4; Length 1050;
Best Local Similarity 65.9%; Pred. No. 5.8e-43;
Matches 375; Conservative 0; Mismatches 193; Indels 1; Gaps 1;

Qy 92 CGCCCTTTCCCTGGGGGCGTGTGGCGGTGACCGCTGTGTGCTGTGCTGTGCTGTCG 151
Db 56 CGCTGTTCCTGGCGCGCTGTGGCGGTGACCGCACCTGTGTGCTGTGCTGTGCTGCG 115

Qy 152 TCGGGGTGAGCGCAACGTGTGACCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGGA 211
Db 116 TGGGCGTGGCGGCAACCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 175

Qy 212 CCACACCAACTTGTACCTGGGAGCATGGCGGTGTCGACCTACTCATCTCTGCTGCGGC 271
Db 176 CCACACCAACTTGTACCTGGGAGCATGGCGGTGTCGACCTACTCATCTCTGCTGCA 235

Qy 272 TGGCGTTCGACCTGTACCGCTCTGGCGCTCGCGGCTTGGGTGTTTCGGGCGCTGCTCT 331
Db 236 TGGCGTTCGACCTGTGGTGGCTGTGGCAGTACCGGCTTGGACCTTTCGGGCGACCTGCTCT 295

Qy 332 GCGGCTTCTCTTACCTGGGCGAGGCTGACCTAGCCACGCTGTGCAATGACGCG 391
Db 296 GCAAACTTCTCAGTTCTGGAGCGAGGCTGACCTAGCCACGCTGTCTACCATCACGG 355

Qy 392 CGCTCAGGCTCGAGGCTACTTGGCCATCTGGCGCTCGCGGCTCGCGGCTGCTGTGCTCA 451
Db 356 CGCTCAGGCTCGAGGCTACTTTCGCACTCTGCTTCCCGCTCGCGGCTGCTGTGCTGA 415

Qy 452 CCGGCGCGGCTCGCGGCTCATGCTGTGCTGTGCGGCTGCGGCTGCTGTGCGGCTCTCTGCG 511
Db 416 CCAAGGCGCGCTGAAGCTGCGCTTCTGGGCTGCTGGGCTGCTGTGCGGCTCTCTGCGGCT 475

Qy 512 GTCCCTTCTTCTTCTGCTGGGCTGAGCAGGACCCCGGCTATC-TCCGTAGTCTCCGCGC 570
Db 476 GGCCCATCTTCTGCTGTGGGCTGAGCAGGACCGGACCGGACCGGACCGGACCGG 535

Qy 571 CTCAATGCAACCGCGGATCGCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 630
Db 536 CGGAGTGGCGGCGCACCGAGTTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGG 595

Qy 631 TCGGCGGCGCGCACCGCTTCTCCCGCGCTC 659
Db 596 TGTCCAGCGCTTCTTCTTCTTCTGCGCGCTC 624

RESULT 5

US-09-077-675A-1
; Sequence 1, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:


```

RESULT 8
US-09-743-475-1
; Sequence 1, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ IDS: 10

```


Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPINOT01
CLONE: 2018536
US-09-016-434-359

Query Match 16.5%; Score 229; DB 4; Length 250;
Best Local Similarity 98.8%; Pred. No. 4.6e-39;
Matches 240; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1148 TCTCAGTACTTTAAACATCGTCGCTCTGCAACTTTTCTATCTGAGGCGCATCTATCAACCCA 1207
Db 1 TCTCAGTACTTTAAACATCGTCGCTCTGCAACTTTTCTATCTGAGGCGCATCTATCAACCCA 60
QY 1208 ATCTCTTACAACCTATTTCAAAGAGTACAGAGCGCGGCGCTTTAAACTGCTGCTCGCA 1267
Db 61 ATCTCTTACAACCTATTTCAAAGAGTACAGAGCGCGGCGCTTTAAACTGCTGCTCGCA 120
QY 1268 AGGAGTCCAGCGCGGAGGCTTCCACAGACGAGGACACTGCGGGGAGTTTCAGGG 1327
Db 121 AGGAGTCCAGCGCGGAGG- TTCCACAGACGAGGACACTGCGGGGAGTTTCAGGG 179
QY 1328 GACACTGGAGGAGACACGCTGGGCTACACCGAGACAAGCGCTTAAAGTGAAGACGATGGGA 1387
Db 180 GACACTGGAGGAGACACGCTGGGCTACACCGAGACAAGCGCTTAAAGTGAAGACGATGGGA 239
QY 1388 TAA 1390
Db 240 TAA 242

RESULT 12
US-09-077-675A-9
; Sequence 9, Application US/09077675A

Patent No. 6242199
GENERAL INFORMATION:
APPLICANT: Pai, Lee-Yuh
APPLICANT: Feighner, Scott C.
APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
FILING DATE: 3-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19590P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-077-675A-9

Query Match 16.5%; Score 228.8; DB 3; Length 1122;
Best Local Similarity 57.9%; Pred. No. 6.9e-39;
Matches 424; Conservative 0; Mismatches 307; Indels 1; Gaps 1;
QY 93 GCCCTTTCCCTGGGGCGCTGGTGCCCGTGACCGCTGTGTGCCTGTGCTGTTCGTGT 152
Db 360 GCTCTTCCCGCGCGCTGCTGGGGCGGTACAGCCACCTGCGTGGCACCTCTTCGTGT 419
QY 153 CGGGGTGAGCGGCAACGTGGTGACCGTGATGTCGGGGCGCTACCGGACATCGGCAC 212
Db 420 GGGTATCGCTGGCAACCTGCTCACCATGCTGGTGGTGTGCGGCTTCCGCGAGCTGCGAC 479
QY 213 CACCACCAACTTGTACCTGGCGAGCATGGCGCTGTCGACCTACTCATCTGCTCGGGCT 272
Db 480 CACCACCAACTTGTACCTGTCAGATGGCCCTTCTCCGATCTGCTCATCTTCTCTGAT 539
QY 273 GCCGTTCGACCTTACCGCCCTCTGGCGCTCGCGGCGCTGGGGTGTTCGGGCGCGCTCTG 332
Db 540 GCCCTTGGACCTCGTTCGCTTGGCAGTACCGGCGCTTGGAACTTCCGCGGACCTCTCTG 599
QY 333 CGGCTGTGCTCTTACGTGGGGGAGGCTGACACTTACGCCACGCTGTGTCGACATGACCGC 392
Db 600 CAAACTCTTCCAATTCGTTCAGTGAGCTGACCTTACGCCACGCTGTGTCGACATGACGAC 659
QY 393 GCTCAGCTCGAGCGCTACCTGGCCCATCTGGCGCGCTCGCGCGCGCTCTTCTGTCAC 452
Db 660 GCTGAGCGTGGAGCGCTACTTCCGCGCTTCTGCTTCCCACTCCGCGGCGCAAGGTGGTGTGTCAC 719

QY 453 CCGGCGCCGCGTCCGCGGCTCATCGCTGTGCTCTGGGCGCGTGGCTCTCTCTGCGCG 512
Db 720 CAAGGGGCGGTGAAGCTGCTCATCTTCTGCTCATCTGGGCGGTGGCTCTCTGAGCGCGG 779
QY 513 TCCTTCTTGTCTGCTGGTGGGCTGAGCAGAGAACCGCGCATCT-CCGTAGTCCGCGGC 571
Db 780 GCCCATCTTCTGCTAGTGGGCTGAGCAGAGAACCGCATCTTGGGACACCAA 839
QY 572 TCAATGGACCGCGGATCGCTCTCGCTCTCTGCTCTGCTCTGCTCTCTGCTCT 631
Db 840 CAGATGCGCGCCACCGAGTTGGGCTGGCTCTGCTCTGCTCTGCTCTGCTCT 899
QY 632 CCGGCGCGCACCGCGCTCCCGCGCTGGGCGCGGAGACCGCGCGCGCTGT 691
Db 900 GTCCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 959
QY 692 TCAGCGCGAATGCGCGCGCGAGCCCGCGCTGCTGCTGCTGCTGCTGCTGCT 751
Db 960 CAGGAAGCTGTGGCGGAGGAGCGCGCGATCTGCTGCTGCTGCTGCTGCT 1019
QY 752 TCACACCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 811
Db 1020 GAACACAAAGAAACCGTGAAATGCTGGTGGGCTCAGCGCGCTCAGCGCTTCTCT 1079
QY 812 GCGGCGAGCTGT 823
Db 1080 CCGGCGCTCTAT 1091

RESULT 13

US-09-077-674-9
; Sequence 9, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,674
; FILING DATE: 3-JUN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19589P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1122 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-077-674-9
Query Match 16.5%; Score 228.8; DB 4; Length 1122;
Best Local Similarity 57.9%; Pred. No. 6.9e-39;
Matches 424; Conservative 0; Mismatches 307; Indels 1; Gaps 1;
QY 93 GCCCTTCCCTGGGCGGCTGGTCCGCTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 152
Db 360 GCTCTTCCCGCGCGCTGCTGGCGGCGTACAGCCACCTGCGTGGGACTCTTCTGCTGCT 419
QY 153 CGGGGTGAGCGCAACGTGGTGACCTGATCGGCGCTACCGGCGCTACCGGCGATCGCGAC 212
Db 420 GGGTATCGCTGGCAACCTGCTCACATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 479
QY 213 CACCACCAACTTGTACCTGGGCGAGCATGGCGCTGTCCGACCTACTCATCTCTGCTGGGCT 272
Db 480 CACCACCAACTTGTACCTGGGCGAGCATGGCGCTGTCCGATCTGCTCATCTTCTCTGCT 539
QY 273 GCGTTCGACCTGTACCGCTCTGCGGCTCGCGGCTGGTGGTGGTGGTGGTGGTGGTGGT 332
Db 540 GCGCTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
QY 333 CCGCTGCTCTACGTGGGCGAGGCTGACCTACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 392
Db 600 CAACTCTTCAATTCGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 659
QY 393 GCTCAGCGTGGGCGCTACCTGGGCGATCTGCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCT 452
Db 660 GCTGAGCGTGGGCGCTACCTGGGCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
QY 453 CCGGCGCGCTGCTGCGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
Db 720 CAAGGGCGGCTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 779
QY 513 TCCTTCTTCTGCTGGTGGGCTGAGCAGAGCGCGCGCATCT-CCGTAGTCCCGGCGC 571
Db 780 GCCCATCTTCTGCTAGTGGGCTGAGCAGAGCGCGCGCATCT-CCGTAGTCCCGGCGC 839
QY 572 TCAATGGCACCGCGGATCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 631
Db 840 CGAGTGGCGCGCCACCGAGTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
QY 632 CCGGCGCGCACCGCGCTCCCGCGCTGGGCGCGGAGACCGCGGAGCGCGGCGGCTGT 691
Db 900 GTCCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 959
QY 692 TCAGCGCGAATGCGGCGGAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
Db 960 CAGGAGCTGTGGCGGAGGAGCGCGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019
QY 752 TCACCACCGCTACTTCTTCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
Db 1020 GAACCAAGCAACCGTGAATGCTGGTGGGCTCAGCGCGGCTCAGCGCTTCTCT 1079
QY 812 GCGGCGAGCTGT 823
Db 1080 CCGGCGCTCTAT 1091

RESULT 14

US-09-077-675A-15
; Sequence 15, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.

[illegible]

Db	344	GCAAACTCTTCCAGTCTTTGTACGAGAGCTGCACCTACGCCACGGTCTCTCAACATCACCG	403
Qy	392	CGCTCAGGTCGAGGGTACTCTGGCCATCTCGCCCGCTCCGGCCCGCGTCTTGTC	451
Db	404	CGCTGAGGTCGAGCGTACTTCCGCCATCTGCTTCCCTCTCGGGCCAAAGTGGTGGTCA	463
Qy	452	CCGGCGCGCGTCCGGCGCTCATCGTGTGCTCTGGCCGTCGGCGTCTCTCTGCGG	511
Db	464	CTAAGGGCCGCGTGAAGCTGTGCATCTTGTGCATCTGGCGCGTGGCTTCTTGCAAGCGCGG	523
Qy	512	GTCCTTCTTGTCTCTGGTGGCGTCGAGCAGGACCCCGCA	553
Db	524	GGCCCATCTCTGTCGTCTGGTGGCGTGGAGCAGCAAAACGGCA	565

Search completed: April 11, 2005, 13:13:33
Job time : 229.453 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1161	83.5	1161	18	US-10-679-813-11	Sequence 11, Appl
2	1078	77.6	1239	15	US-10-325-567A-472	Sequence 472, App
3	1078	77.6	1239	15	US-10-290-078-13	Sequence 13, Appl
4	1078	77.6	1239	15	US-10-290-078-14	Sequence 14, Appl
5	1078	77.6	1239	16	US-10-206-677-1	Sequence 1, Appli
6	1078	77.6	1239	18	US-10-679-813-9	Sequence 9, Appli
7	1047.2	75.3	2040	10	US-09-876-252-129	Sequence 129, App
8	1047.2	75.3	2040	17	US-10-417-820A-129	Sequence 129, App
9	1047.2	75.3	2040	18	US-10-723-955-129	Sequence 129, App
10	1040.8	74.9	2040	17	US-10-417-820A-151	Sequence 151, App
11	501.2	36.1	1179	18	US-10-363-145A-3737	Sequence 3737, A

QY 61 GGGCTGCGCCCTTGGAGAGCGCGCTGCTGCCCTTTCCCTTGGGGCGCTGGTGCG 120
DB 61 GGGCTGCGCCCTTGGAGAGCGCGCTGCTGCCCTTTCCCTTGGGGCGCTGGTGCG 120
QY 121 GTGACCGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 GTGACCGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 ATGCTGATCGGGCGCTACCGGACATGCGGACACCACTTGTACTGCGGACGATG 240
DB 181 ATGCTGATCGGGCGCTACCGGACATGCGGACACCACTTGTACTGCGGACGATG 240
QY 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGCTGCGCTGCGCTGCGCTGCG 300
DB 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGCTGCGCTGCGCTGCGCTGCG 300
QY 301 TCGCGCCCTGCGGTGCTGCGGCGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTG 360
DB 301 TCGCGCCCTGCGGTGCTGCGGCGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTG 360
QY 361 TGCACCTAGCCACGCTGTGACATGACCGGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 TGCACCTAGCCACGCTGTGACATGACCGGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 TGCAGCCCGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 TGCAGCCCGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 GTGCTGTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 GTGCTGTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 CAGGACCCCGCATCTCGGTAGTCCGGGCTCAATGGACCGCGGATGCGCTCTCG 600
DB 541 CAGGACCCCGCATCTCGGTAGTCCGGGCTCAATGGACCGCGGATGCGCTCTCG 600
QY 601 CTTCTGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 601 CTTCTGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 GGGCCCGAGACCGCGGAGCCCGCGCTGTTTCAAGCGGATGCGGCGAGCCCGCG 720
DB 661 GGGCCCGAGACCGCGGAGCCCGCGCTGTTTCAAGCGGATGCGGCGAGCCCGCG 720
QY 721 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 CAGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCG 840
DB 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGCGGAGCTGTGAGCAGCGCGGCG 840
QY 841 CTGCGAGGCGCGGCGCTCGGGCGGAGAGAGCCACCGGACAGCCGTGCGGCTCTG 900
DB 841 CTGCGAGGCGCGGCGCTCGGGCGGAGAGAGCCACCGGACAGCCGTGCGGCTCTG 900
QY 901 CTTAAGTGGAGCGCGGTGGTTCCAAAGAGCGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 CTTAAGTGGAGCGCGGTGGTTCCAAAGAGCGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GGGCAAGCGCTGGGTCCTCTCCCTGCTGCGCCAGCTGTGGGCGCGCTTCCAGTCCC 1020
DB 961 GGGCAAGCGCTGGGTCCTCTCCCTGCTGCGCCAGCTGTGGGCGCGCTTCCAGTCCC 1020
QY 1021 TTTCTATTTCGATTCAGGCTCCACCGCGGTGGTGGTCTTGGCATTTAATTTG 1080
DB 1021 TTTCTATTTCGATTCAGGCTCCACCGCGGTGGTGGTCTTGGCATTTAATTTG 1080
QY 1081 CTGGTGTGCTTCCAGTGGGAGATCATTTTACATAACAGGAGATTCCGGATGAT 1140
DB 1081 CTGGTGTGCTTCCAGTGGGAGATCATTTTACATAACAGGAGATTCCGGATGAT 1140

QY 1141 GTACTTCTCTCAGTACTTTAA 1161
DB 1141 GTACTTCTCTCAGTACTTTAA 1161
RESULT 2
US-10-225-567A-472
; Sequence 472, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 472
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-472
Query Match 77.6%; Score 1078; DB 15; Length 1239;
Best Local Similarity 89.1%; Pred. No. 1.9e-281;
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;
QY 1 ATGGGACGCCCTTGAACGGCAGCAGCGGCCCGCGGGGGCGCGGAGCCCGCTGGGCC 60
DB 1 ATGGGACGCCCTTGAACGGCAGCAGCGGCCCGCGGGGGCGCGGAGCCCGCTGGGCC 60
QY 61 GCGTGGCGGCTTGGCAGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 GCGTGGCGGCTTGGCAGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 ATGCTGATCGGGCGCTACCGGACATGCGGACACCACTTGTACTGCGGACGATG 240
DB 181 ATGCTGATCGGGCGCTACCGGACATGCGGACACCACTTGTACTGCGGACGATG 240
QY 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 GCGGTGTCGACCTACTCATCTGCTGCGGCTGCGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 TCGGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 TCGGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 TGCACCTAGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 TGCACCTAGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 TCGCGCCCGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 TCGCGCCCGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 GTGCTGTGGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 GTGCTGTGGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 CAGGACCCCGCATCTCGGTAGTCCGGGCTCAATGGACCGCGGATGCGCTCTCG 600
DB 541 CAGGACCCCGCATCTCGGTAGTCCGGGCTCAATGGACCGCGGATGCGCTCTCG 600
QY 601 CTTCTGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

Qy 1321 TGCAGGACACTGGAGAGACACGGTGGGCTACACCGAGACAGCGCTAAAGTGAAGAC 1380
Db 1170 TGCAGGAGACACTGGAGAGACACGGTGGGCTACACCGAGACAGCGCTAAAGTGAAGAC 1229
Qy 1381 GATGGGATAA 1390
Db 1230 GATGGGATAA 1239

RESULT 5
US-10-206-677-1
; Sequence 1, Application US/10206677
; Publication No. US20030186336A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences, Inc.
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; APPLICANT: Kulander, Bruce G.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO
; FILE OF INVENTION: GPCR 38, A G PROTEIN-COUPLED RECEPTOR (GPCR)
; FILE REFERENCE: 1920-1-8
; CURRENT APPLICATION NUMBER: US/10/206,677
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/250,251
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,452
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-206-677-1

Query Match 77.6%; Score 1078; DB 16; Length 1239;
Best Local Similarity 89.1%; Pred. No. 1.9e-281;
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;
Qy 1 ATGGGACGCCCTGGAACGGAGACGCGCCCGAGGGGGCGGAGCCCGCTGGGCCC 60
Db 1 ATGGGACGCCCTGGAACGGAGACGCGCCCGAGGGGGCGGAGCCCGCTGGGCCC 60
Qy 61 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGGCGCTGTGCGG 120
Db 61 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGCCCTTTCCCTGGGGGCGCTGTGCGG 120
Qy 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 GTGACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy 181 ATGCTGATCGGGCGCTACGGGACATCGGACACCAACCACTTGTACCTGGGAGCATG 240
Db 181 ATGCTGATCGGGCGCTACGGGACATCGGACACCAACCACTTGTACCTGGGAGCATG 240
Qy 241 GCGGTGTCGACCTACTACTCTGCTGCGGCTGCGCTGCGCTGCGCTGCGCTGCGGCG 300
Db 241 GCGGTGTCGACCTACTACTCTGCTGCGGCTGCGCTGCGCTGCGCTGCGCTGCGGCG 300
Qy 301 TCGGCGCCCTGGGTTTCGGGCGCGTGTCTGCTGCGGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TCGGCGCCCTGGGTTTCGGGCGCGTGTCTGCTGCGGCTGCTGCTGCTGCTGCTGCTG 360
Qy 361 TGCACCTAGCCACCGCTGCTGACATGACCGGCTCAGGCTCAGGCTACCTGGCCATC 420
Db 361 TGCACCTAGCCACCGCTGCTGACATGACCGGCTCAGGCTCAGGCTACCTGGCCATC 420
Qy 421 TCGCGCCCGCTCCGCGCGCGCTTGTGTCACCGCGCGCGCTCCGCGCGCTCATCGCT 480
Db 421 TCGCGCCCGCTCCGCGCGCGCTTGTGTCACCGCGCGCGCTCCGCGCGCTCATCGCT 480
Qy 481 GTGCTCTGGGCGCGTGGCGCTGCTCTCTGCGCGGCTCCCTTTCTTGTCTCTGCTGGGCGTGGAG 540

Db 481 GTGCTCTGGGCGGTGGGCGCTGCTCTCTGCGCGTCCCTTTCTTGTCTCTGGTGGGCGTGGAG 540
Qy 541 CAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGGACCCCGCGGATCGCTCTCTCG 600
Db 541 CAGGACCCCGGCATCTCCGTAGTCCCGGGCTCAATGGACCCCGCGGATCGCTCTCTCG 600
Qy 601 CCTCTGCGCTCTGCTGCGCGCTCTCTGCGGCGGCGCACCGCGCTCCCGCGCTCG 660
Db 601 CCTCTGCGCTCTGCTGCGCGCTCTCTGCGGCGGCGCACCGCGCTCCCGCGCTCG 660
Qy 661 GGGCCGAGACCCGCGGAGCGCGCGCTGTTAGCGCGGAATGCCGCGAGCCCGCG 720
Db 661 GGGCCGAGACCCGCGGAGCGCGCGCTGTTAGCGCGGAATGCCGCGAGCCCGCG 720
Qy 721 CAGCTGGGCGCGCTGCGCTGCTCATGCTGTGGGTACCCACCGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGGCGCGCTGCGCTGCTCATGCTGTGGGTACCCACCGCTACTTCTTCTGCGCTTT 780
Qy 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGAGTGTGAGAGAGCGCGGCGG 840
Db 781 CTGTGCTCAGCATCTCTACGGGCTCATCGGGGAGAGTGTGAGAGAGCGCGGCGG 840
Qy 841 CTGCGAGCGCGCGCGCTCGGGGCGGAGAGCGCACCGGAGACCGTCCGCGTCTG 900
Db 841 CTGCGAGCGCGCGCGCTCGGGGCGGAGAGAGCGCACCGGAGACCGTCCGCGTCTG 900
Qy 901 CGTAAGTGGAGCGCGCTGGTTCGAAAGACCGCTGCTGCGCGCGCGCGCGGAGCC 960
Db 901 C----- 901
Qy 961 GCGCAAAAGCTGGGTGCCCTTCCCTGCTGCGCCAGCTCTGGGCGCGCTTCCAGCTCCC 1020
Db 902 ----- 901
Qy 1021 TTTCTATTTCGATTCCAGCTCCACCGCGCTGCTGGTGGTCTGGCATTTATAATTG 1080
Db 902 -----TGGTGGTGGTCTGGCATTTATAATTG 929
Qy 1081 CTGGTTGCCCTTCCAGCTTGGCAGATCATTTATATAACGAGAGATTTCGCGGATGAT 1140
Db 930 CTGGTTGCCCTTCCAGCTTGGCAGATCATTTATATAACGAGAGATTTCGCGGATGAT 989
Qy 1141 GTACTTCTCAGTACTTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 990 GTACTTCTCAGTACTTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049
Qy 1201 CAACCCAACTCTTCAACCTCATTTCAAGAGTACAGAGCGGCGCTTTAACTGCT 1260
Db 1050 CAACCCAACTCTTCAACCTCATTTCAAGAGTACAGAGCGGCGCTTTAACTGCT 1109
Qy 1261 GCTCGAAGGAGTCCAGGCGGAGGCTTCCAGAGAGGAGGACACTGCGGGGAGT 1320
Db 1110 GCTCGAAGGAGTCCAGGCGGAGGCTTCCAGAGAGGAGGACACTGCGGGGAGT 1169
Qy 1321 TGCAGGGGACACTGGAGGAGACAGCTGGGCTACACCGAGACAAGCGCTAAAGTGAAGAC 1380
Db 1170 TGCAGGGGACACTGGAGGAGACAGCTGGGCTACACCGAGACAAGCGCTAAAGTGAAGAC 1229
Qy 1381 GATGGGATAA 1390
Db 1230 GATGGGATAA 1239

RESULT 6
US-10-679-813-9
; Sequence 9, Application US/10679813
; Publication No. US20040208866A1
; GENERAL INFORMATION:
; APPLICANT: JASPER, STEPHEN R.
; APPLICANT: SHEPPARD, PAUL O.
; APPLICANT: BISHOP, PAUL D.
; APPLICANT: KUIJPER JOSEPH L.

APPLICANT: DEISHER, THERESA A.
; TITLE OF INVENTION: METHODS OF REGULATING BODY WEIGHT
; FILE REFERENCE: 02-23
; CURRENT APPLICATION NUMBER: US/10/679,813
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/416,918
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-679-813-9

Query Match 77.6%; Score 1078; DB 18; Length 1239;
Best Local Similarity 89.1%; Pred. No. 1.9e-281;
Matches 1239; Conservative 0; Mismatches 0; Indels 151; Gaps 1;
QY 1 ATGGGAGCCCTTGAAACGGAGAGCAGCGCCCGAGGGGGCGCGGAGCGCCGCTGGGCC 60
Db 1 ATGGGAGCCCTTGAAACGGAGAGCAGCGCCCGAGGGGGCGCGGAGCGCCGCTGGGCC 60
QY 61 GCGCTGCGCCCTTGAGAGAGCGCGCTGCTGCCCTTTCCCTCGGGGGCGCTGGTGGCG 120
Db 61 GCGCTGCGCCCTTGAGAGAGCGCGCTGCTGCCCTTTCCCTCGGGGGCGCTGGTGGCG 120
QY 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 180
Db 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 180
QY 181 ATGCTGATGGCGGCTACCGGAGATGCGGACACACAACTTGTAATCTGGGAGAGATG 240
Db 181 ATGCTGATGGCGGCTACCGGAGATGCGGAGACACCACTTGTAATCTGGGAGAGATG 240
QY 241 GCGGTGTCGACCTACTATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 300
Db 241 GCGGTGTCGACCTACTATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 300
QY 301 TCGCGCCCTTGGGTGTTGGGCGCTGTCTGCGCGCTGTCTGCGCGCTGTCTGCGCGCT 360
Db 301 TCGCGCCCTTGGGTGTTGGGCGCTGTCTGCGCGCTGTCTGCGCGCTGTCTGCGCGCT 360
QY 361 TGCACCTAGCCACGCTGTCATGACATGACCGGCTCAGGTCGAGCGCTACCTGGCCATC 420
Db 361 TGCACCTAGCCACGCTGTCATGACATGACCGGCTCAGGTCGAGCGCTACCTGGCCATC 420
QY 421 TCGCGCCGCTCGCGCGCGCTCTTGGTACCGCGCGCGCTCGCGCGCTCATGCT 480
Db 421 TCGCGCCGCTCGCGCGCGCTCTTGGTACCGCGCGCGCTCGCGCGCTCATGCT 480
QY 481 GTGCTGTGGCGCGTGGCGCTGTCTGCGCGCTCCCTTTCTTGTCTGCTGGGCGTGGAG 540
Db 481 GTGCTGTGGCGCGTGGCGCTGTCTGCGCGCTCCCTTTCTTGTCTGCTGGGCGTGGAG 540
QY 541 CAGGACCCCGGATCTCGTAGTCCGGGCTCAATGACCGCGCGGATCGCTCCCTCG 600
Db 541 CAGGACCCCGGATCTCGTAGTCCGGGCTCAATGACCGCGCGGATCGCTCCCTCG 600
QY 601 CCTCTCGCTCGTGGCGCGCTCTGCTGTCTGCGGGCGCACCGCGCTCGCGCGCTCG 660
Db 601 CCTCTCGCTCGTGGCGCGCTCTGCTGTCTGCGGGCGCACCGCGCTCGCGCGCTCG 660
QY 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTGTCAGCGCGAATGCGGCGAGCGCCGCG 720
Db 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTGTCAGCGCGAATGCGGCGAGCGCCGCG 720
QY 721 CAGCTGGGCGCGCTGGGTGCTATGCTGTGGGTGACACCGGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGGCGCGCTGGGTGCTATGCTGTGGGTGACACCGGCTACTTCTTCTGCGCTTT 780

QY 781 CTGTGCTTCAGCATCCTCTACGGGCTCATCGGGGGAGGCTGTGAGCAGCCGGCGCG 840
Db 781 CTGTGCTTCAGCATCCTCTACGGGCTCATCGGGGGAGGCTGTGAGCAGCCGGCGCG 840
QY 841 CTGGAGGCGCGCGCGCTCGGGGGAGAGAGCCACCGGCGAGACCGCTCGCGGTCTG 900
Db 841 CTGGAGGCGCGCGCGCTCGGGGGAGAGAGCCACCGGCGAGACCGCTCGCGGTCTG 900
QY 901 CGTAAGTGGAGCGCGCTGTGTTCCAAAGACGCTGCTGCAGTCCGCCCGCGGGGACC 960
Db 901 C----- 901
QY 961 GCGCAAGCGTGGGTGCCCTTCCCTGCTGCCCGAGCTCTGGGCGCGCTTCCAGCTCCC 1020
Db 902 ----- 901
QY 1021 TTTCCTATTTCCGATTCAGCCTCCACCGCGCTGCGGTGTGCTGTGCTTGTGCAATTAATAATTG 1080
Db 902 -----TGTTGGTGTCTGGCAATTAATAATTG 929
QY 1081 CTGTTGCGCTTCACGTTGGCAGAAATCATTTACATAAACAAGAAATTCGCGGATGAT 1140
Db 930 CTGTTGCGCTTCACGTTGGCAGAAATCATTTACATAAACAAGAAATTCGCGGATGAT 989
QY 1141 GTACTTCTCAGTACTTTAAACATCGTCTGCAACTTTTCTATCTGAGCGCATCTAT 1200
Db 990 GTACTTCTCAGTACTTTAAACATCGTCTGCAACTTTTCTATCTGAGCGCATCTAT 1049
QY 1201 CAACCCAACTCTTCAACCTCAATTTCAAAGAAGTACAGAGCGCGCGCTTTAAACTGCT 1260
Db 1050 CAACCCAACTCTTCAACCTCAATTTCAAAGAAGTACAGAGCGCGCGCTTTAAACTGCT 1109
QY 1261 GCTCGAAGAAAGTCCAGGCGGAGAGGCTTCCACAGAAGCAGGACACTCGCGGGGAAGT 1320
Db 1110 GCTCGAAGAAAGTCCAGGCGGAGAGGCTTCCACAGAAGCAGGACACTCGCGGGGAAGT 1169
QY 1321 TGACGGGACACTCGAGGAGACAGCGTGGGTACCCGAGACAGCGCTAACGTGAAGAC 1380
Db 1170 TGACGGGACACTCGAGGAGACAGCGTGGGTACCCGAGACAGCGCTAACGTGAAGAC 1229
QY 1381 GATCGGATAA 1390
Db 1230 GATCGGATAA 1239

RESULT 7

US-09-876-252-129
; Sequence 129, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

;; TITLE OF INVENTION: Receptors
;; FILE REFERENCE: 7.US28.CON
;; CURRENT APPLICATION NUMBER: US/10/417,820A
;; CURRENT FILING DATE: 2003-04-16
;; PRIOR APPLICATION NUMBER: 09/416,760
;; PRIOR FILING DATE: 1999-10-12
;; PRIOR APPLICATION NUMBER: 09/170,496
;; PRIOR FILING DATE: 1998-10-13
;; PRIOR APPLICATION NUMBER: 60/110,060
;; PRIOR FILING DATE: 1998-11-27
;; PRIOR APPLICATION NUMBER: 60/120,416
;; PRIOR FILING DATE: 1999-02-16
;; PRIOR APPLICATION NUMBER: 60/121,852
;; PRIOR FILING DATE: 1999-02-26
;; PRIOR APPLICATION NUMBER: 60/109,213
;; PRIOR FILING DATE: 1998-11-20
;; PRIOR APPLICATION NUMBER: 60/123,944
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 60/123,945
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 60/123,948
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 60/123,951
;; PRIOR FILING DATE: 1999-03-12
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 155
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 129
;; LENGTH: 2040
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-417-820A-129

Query Match 75.3%; Score 1047.2; DB 17; Length 2040;
Best Local Similarity 99.7%; Pred. No. 4.5e-273; Mismatches 3; Indels 0; Gaps 0;
Matches 1049; Conservative 0;

QY 1 ATGGGAGCGCCCTGGAAAGCGGACGCGCGCCCGGAGGGGGGCGGAGCGCGGTGGGCC 60
Db 1 ATGGGAGCGCCCTGGAAAGCGGACGCGCGCCCGGAGGGGGGCGGAGCGCGGTGGGCC 60
QY 61 GCGCTGCGCGCTTGGGAGCGCGCGTGTGCGCCCTTTCCCTGGGGGCGGTGTGCGCG 120
Db 61 GCGCTGCGCGCTTGGGAGCGCGCGTGTGCGCCCTTTCCCTGGGGGCGGTGTGCGCG 120
QY 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
Db 121 GTGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
QY 181 ATGCTGATCGGGCGCTACCGGACATCGGACACACCACTTGTACCTTGGGAGCATG 240
Db 181 ATGCTGATCGGGCGCTACCGGACATCGGACACCACTTGTACCTTGGGAGCATG 240
QY 241 GCGGTGTGCGACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 300
Db 241 GCGGTGTGCGACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 300
QY 301 TCGCGCCCTGGGTGTGGGGCGGTGTGCGCCCGGTGTGCGCCCGGTGTGCGCCCGGTGTG 360
Db 301 TCGCGCCCTGGGTGTGGGGCGGTGTGCGCCCGGTGTGCGCCCGGTGTGCGCCCGGTGTG 360
QY 361 TGCACCTAGCCACGCTGTGTCACATGACCGGGCTCAGCGTGTGAGCGGTACTTGGCCATC 420
Db 361 TGCACCTAGCCACGCTGTGTCACATGACCGGGCTCAGCGTGTGAGCGGTACTTGGCCATC 420
QY 421 TCGCGCCCGCTCGCGCGCGGTCTTGTACCGCGCGCGGTCTCGCGCGGTCTATCGCT 480
Db 421 TCGCGCCCGCTCGCGCGCGGTCTTGTGTACCGCGCGCGGTCTCGCGCGGTCTATCGCT 480
QY 481 GTGCTGTGGGCGGTGGCGGTGTGCTGTGCGCGGTCTTGTGCTGCTGTGCTGTGCTGTGCT 540
Db 481 GTGCTGTGGGCGGTGGCGGTGTGCTGTGCGCGGTCTTGTGCTGCTGTGCTGTGCTGTGCT 540

QY 541 CAGGACCCCGCATCTCCGTAGTCCCGGCGCTCAATGGCACCCGCGCGGATCGCTCTCTCG 600
Db 541 CAGGACCCCGCATCTCCGTAGTCCCGGCGCTCAATGGCACCCGCGCGGATCGCTCTCTCTCG 600
QY 601 CCTCTCGCTCGTTCGCGCGCTCTCTGTGCTCTCGCGGGGCGCACCGCGGTCTCCCGCGTCTG 660
Db 601 CCTCTCGCTCGTTCGCGCGCTCTCTGTGCTCTCGCGGGGCGCACCGCGGTCTCCCGCGTCTG 660
QY 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTGTAGCGCGGAAATCGCGCGGAGCCCGCGCG 720
Db 661 GGGCCCGAGACCGCGGAGCGCGCGCTGTGTAGCGCGGAAATCGCGCGGAGCCCGCGCG 720
QY 721 CAGCTGGGCGCGCTGCGGTGTATGCTGTGGGTCAACACCGCTACTTCTTCTGCGCTTT 780
Db 721 CAGCTGGGCGCGCTGCGGTGTATGCTGTGGGTCAACACCGCTACTTCTTCTGCGCTTT 780
QY 781 CTGTGCTCAGCATCTCTACGGCTCATCGGGCTCATCGGGGAGAGTGTGGAGCAGCGCGGCG 840
Db 781 CTGTGCTCAGCATCTCTACGGCTCATCGGGGAGAGTGTGGAGCAGCGCGGCGCG 840
QY 841 CTGCGAGCGCGCGCGCTCGGGGAGAGAGCGCACCGGAGAGCGGAGAGCGGAGCGGCG 900
Db 841 CTGCGAGCGCGCGCGCTCGGGGAGAGAGCGCACCGGAGAGCGGAGAGCGGAGCGGCG 900
QY 901 CGTAAGTGGAGCGCGCGTGTGTTCCAAAGACGCGCTGCGAGTCCGCGCGCGCGGAGCG 960
Db 901 CGTAAGTGGAGCGCGCGTGTGTTCCAAAGACGCGCTGCGAGTCCGCGCGCGCGGAGCG 960
QY 961 GCGGAGCGGTGGGTGCGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 GCGGAGCGGTGGGTGCGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 TTTCTCTATTTTCGATTCAGCTCCACCGCGCG 1052
Db 1021 TTTCTCTATTTTCGATTCAGCTCCACCGCGCG 1052

RESULT 9
US-10-723-955-129
; Sequence 129, Application US/10723955
; Publication No. US20040110238A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lehman-Bruinema, Karin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Gore, Martin
; APPLICANT: White, Carol
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US29.CON
; CURRENT APPLICATION NUMBER: US/10/723,955
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 10/417,820
; PRIOR FILING DATE: 2003-4-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12

QY		841	CTGCGAGGGCCGGCCGCCCTCTGGGGCGGAGAGAGGCACCGGAGACCGTTCGCGTGCTTG	900
Db		841	CTGCGAGGGCCGGCCGCCCTCTGGGGCGGAGAGAGGCACCGGAGACCGTTCGCGTGCTTG	900
QY		901	CGTAAGTGGAGCGCGCGTGTGTTCCAAGAAGCGCCTGCTGCAGTCCGCGCCCGCGGGAGCC	960
Db		901	CGTAAGTGGAGCGCGCGTGTGTTCCAAGAAGCGCCTGCTGCAGTCCGCGCCCGCGGGAGCC	960
QY		961	GCGCAAAACGCTGGGTCCCCCTTCCCCTGTGCGCCACGCTCTTGGCGCGCGTTCAGGTCCC	1020
Db		961	GCGCAAAACGCTGGGTCCCCCTTCCCCTGTGCGCCACGCTCTTGGCGCGCGTTCAGGTCCC	1020
QY		1021	TTTTCTATTTCGATTCACAGCTCCACC CGCG 1052	
Db		1021	TTTTCTATTTCGATTCACAGCTCCACC CGCG 1052	
 RESULT 10 US-10-417-820A-151				
; Sequence 151, Application US/10417820A				
; Publication No. US20030229216A1				
; GENERAL INFORMATION:				
; APPLICANT: Chen, Ruoping				
; APPLICANT: Liaw, Chen W.				
; APPLICANT: Lowitz, Kevin				
; APPLICANT: Chalmers, Derek T.				
; APPLICANT: Behan, Dominic P.				
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled				
; TITLE OF INVENTION: Receptors				
; FILE REFERENCE: 7.US28.CON				
; CURRENT APPLICATION NUMBER: US/10/417,820A				
; CURRENT FILING DATE: 2003-04-16				
; PRIOR APPLICATION NUMBER: 09/416,760				
; PRIOR FILING DATE: 1999-10-12				
; PRIOR APPLICATION NUMBER: 09/170,496				
; PRIOR FILING DATE: 1998-10-13				
; PRIOR APPLICATION NUMBER: 60/110,060				
; PRIOR FILING DATE: 1998-11-27				
; PRIOR APPLICATION NUMBER: 60/120,416				
; PRIOR FILING DATE: 1999-02-16				
; PRIOR APPLICATION NUMBER: 60/121,852				
; PRIOR FILING DATE: 1999-02-26				
; PRIOR APPLICATION NUMBER: 60/109,213				
; PRIOR FILING DATE: 1998-11-20				
; PRIOR APPLICATION NUMBER: 60/123,944				
; PRIOR FILING DATE: 1999-03-12				
; PRIOR APPLICATION NUMBER: 60/123,945				
; PRIOR FILING DATE: 1999-03-12				
; PRIOR APPLICATION NUMBER: 60/123,948				
; PRIOR FILING DATE: 1999-03-12				
; PRIOR APPLICATION NUMBER: 60/123,951				
; PRIOR FILING DATE: 1999-03-12				
; Remaining Prior Application data removed - See File Wrapper or PALM.				
; NUMBER OF SEQ ID NOS: 155				
; SOFTWARE: PatentIn version 3.2				
; SEQ ID NO 151				
; LENGTH: 2040				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-417-820A-151				
 Query Match 74.9%; Score 1040.8; DB 17; Length 2040;				
Best Local Similarity 99.3%; Pred. No. 2.4e-271;				
Matches 1045; Conservative 0; Mismatches 7; Indels 0; Gaps 0;				
QY		1	ATGGGAGCCCTTGGAACGCGACGCGCCCGAGGGGCGCGGGAGCGCGGTGGCCCC	60
Db		1	ATGGGAGCCCTTGGAACGCGACGCGCCCGAGGGGCGCGGGAGCGCGGTGGCCCC	60
QY		61	GGCTCGCGCTTGCACAGCGCCGCTGCTGCGCCCTTTCCCTCTGGGGCGCTGGTGCCG	120
Db		61	GGCTCGCGCTTGCACAGCGCGCGCTGCTGCGCCCTTTCCCTCTGGGGCGCTGGTGCCG	120


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US-10-363-345A-33738
; Sequence 33738, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363.345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33738
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 33738
US-10-363-345A-33738

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Query Match	36.1%	Score 501.2	DB 18	Length 1179
Best Local Similarity	79.9%	Pred. No. 2.2e-125		
Matches 590	Conservative 0	Mismatches 148	Indels 0	Gaps 0
QY	1	ATGGGACGCCCTCGAAGCGGACGCGGCCCGAGGGGGCGGGAGCGCGCGTGGCCC	60	
DB	442	ATAAACACCCCTAAACAGCAACGCGCCCGGAAAAAAGCGGAAACCGCGGTAAACC	501	
QY	61	CGCGTGGCGCTTCGACGAGCGCGCTGTCTCGCCCTTTCCTTCGGGGCGCTGGTGGC	120	
DB	502	CGCGTACCGCTTACGACGACGCGCTACTCGCCCTTTCCTTAAACGCTAATACCG	561	
QY	121	GTGACCGCTGTGTCCTGTGCTGCTGTCGCGGGTGAAGGGAACGTGGTGAACGCTG	180	
DB	562	ATACCGCTATATACCTATACCTATTGCTGCTGAAATAAACGACCAACGTAAATACCG	621	
QY	181	ATGCTGATCGGGCGCTACGGGACATCGGACACCAACCACTTGTACTCGGAGCATG	240	
DB	622	ATACTAATCGAACGCTACCGAAACATACGAACCAACCACTTATACCTAAACAAACA	681	
QY	241	CGCGTTCGACCTACTCATCTCTCGGGTGCCTGTTCGACCTGTACCGCTCTGGCGC	300	
DB	682	ACCGTATCGACCTACTCATCTACTCGAACTACCGTTCGACCTATACCGCTCTAAGC	741	
QY	301	TCGGGCGCTGGGTGTTGGGCGCGTGTCTGCGCGCTGTCCCTCTACTGGGGAGGAGC	360	
DB	742	TCGCGACCCCTAAATATTGGAACCGCTACTCTACCGCGCTATCCCTCTACGTAAACG	801	
QY	361	TGACCTACGCCACGCTGTGCACATGACCGCGCTCAGGCTCGAGCGTACTCTGGCCATC	420	
DB	802	TACACCTACGCCACGCTACTACATACCGCGCTCAACGTCTGAAACGCTACTCTAACCA	861	
QY	421	TGCGCCCGCTCCGCGCGCGCTCTTGGTCAACCGGCGCCGCGTCCGCGCTCATCGCT	480	
DB	862	TACCGCGCTCCGCGCGCGCTCTTAATCACCCGACGCGCTCGCGCTCATCGCT	921	
QY	481	GTGCTCTGGGCGGTGGGCGTGTCTCTGCGCGTCCCTTCTTGTCTCTGGTGGGCGTCA	540	
DB	922	ATACTCTAAACCGTAAAGCTACTCTCTACCGATCCCTTCTTATTCCTAATAAAGCTGA	981	
QY	541	CAGAACCCGGCATCTCGTAGTCCGGGCTCAATGGCACCGCGCGGATCGCTCTCTCG	600	
DB	982	CAAAACCCCGACATCTCCGTAAATCCCGAACTCAATTAACCCGCGGAAATCGCTCTCT	1041	
QY	601	CCTCTCGCTCTGTCGCGCTCTCTGTGCTCTCGGGGCGCCACCGCGCTCCCGCGCTCG	660	
DB	1042	CCTCTCGCTCTGTCGCGCTCTCTTAATCTCTCGGAACGCCACCGCGTCCCGCGCTCG	1101	
QY	661	GGGCGCGAGACCGCGAGGCGCGCGCTGTTCAGCGCGAATCGCGCGAGCCCCGCG	720	
DB	1102	AAACCCGAAACCGGAAACCGGACGCTATTCAACCGGAATACGACGAAACCGCGCG	1161	

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Qy      721  CAGCTGGGCGCGTGGCT  738
      ||| ||| ||| ||| |||
Db      1162  CAACCTAAACGCGTACGT  1179

RESULT 13
US-10-363-483A-33737/c
; Sequence 33737, Application US/10363483A
; Publication No. US2005006401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,4
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33737
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated
; OTHER INFORMATION: CpG-island No: 33737
US-10-363-483A-33737

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Query Match	36.1%	Score 501.2	DB 19	Length 1179
Best Local Similarity	79.9%	Pred. No. 2.2e-125		
Matches 590	Conservative 0	Mismatches 148	Indels 0	Gaps 0
Qy	1	ATGGGAGCCCTGGAAACGCGACGCGCCCGAGGGGGCGCGGAGCCCGCTGGGCC	60	
Db	738	ATAAACCAACCCCTAAACAGCAACGACCGCCCGGAAAAACGGAACCGCGTAACCC	679	
Qy	61	GGCGTGGCGCTTGGCGAGAGCGCGCTGCTGGCCCTTTCCCTTGGGGGGCTGGTCCG	120	
Db	678	GGCGTACGGCTTACGACGAAACCGCGTACTTGGCCCTTTCCCTTAAAAACGCTAATACG	619	
Qy	121	GTGACCGCTGTGGCGCTGGCGCTTTCGTGCTGGGGGTGAGCGGCAACGTGTGACCCGTG	180	
Db	618	ATAACCGCTATATACCTATATACCTATTTCGTGCTGAAATAACGACAACGTAAATACCGTA	559	
Qy	181	ATGTGATCGGGGGCTACCGGGACATCGGACACCAACCAACTTTGTATCTGGGAGCATG	240	
Db	558	ATACTAATCGAACGCTACCGGAAACATACGAACCAACCAACCTTATACCTAAACAACATA	499	
Qy	241	GGCGTGTCCGAACCTACTCATCTGCTGGGGTGGCGTTTGGACCTGTACCGCTCTGGGGC	300	
Db	498	ACCGTATCCGACCTACTCATCTACTCGAACTACCGTTCGACCTTATACCGCTCTTAACGC	439	
Qy	301	TCGGGGCCCTGGGTGTTTCGGCGCGCTGCTCTGCGCGCTGTCCCTCTACGTGGGCGAGGC	360	
Db	438	TCGGGACCTTAATATATTCGAACCGCTACTCTACCGCTATCCCTCTACGTAACGGAAC	379	
Qy	361	TGCACCTACGCCACGCTGTGCAATAGACCGCGCTCAGCGCTCAGCGCTACTCGGCCATC	420	
Db	378	TACACCTACGCCACGCTACTACACATAACCGCGCTCAACGCTCGAAACGCTACCTAACCATC	319	
Qy	421	TGGCGGCGCTTCGGCGCCGGCTTGGTCAACCGGCGCGCGTTCGGGGGCTCATCGCT	480	
Db	318	TACCGGCGCTTCGGCGCCGGCTTAAATCACCGACGCGCGCTCCGCGGCTCATCGCT	259	
Qy	481	GTGCTCTGGGCGCTGGGGCTGCTCTCTGCGGTCCTCTTGTTCCTTGGTGGGGCTCGAG	540	
Db	258	ATACTCTAACCGTAACGCTACTCTCTACCGATCCCTTCTTATTCCTAATAAAGTCGAA	199	
Qy	541	CAGAACCCCGGCATCTCCGTAGTCCCGGGGCTCAATGGGACCGCGCGGATCGCTCTCTCG	600	
Db	198	CAAAACCCCGACATCTCCGTAAATCCCGAACTCAATAACACCGCGCGAATCGCTCTCTCG	139	

QY 601 CCTCTCGCTGCTCCCGCCCTCTCTGGCTCTGCGGGGCCACCCGCCCTCCCGCCGCTCG 660
Db 138 CCTCTCGCTGCTCCCGCCCTCTCTAACTCTCGGAACGCCACCGCTCCCGCCGCTCG 79
QY 661 GGGCCGAGACCGCGAGCGCGCGCTGTTACGCGCGGATGCGGCGGAGCCCGCG 720
Db 78 AAACCGGAACCGCGAAACCGCGAGCTATTCAACCGGGAATACCGACCGAACCCCGG 19
QY 721 CAGCTGGGCGCGCTCGT 738
Db 18 CAACTAAACGCGCTACGT 1
RESULT 14
US-10-363-483A-33738
; Sequence 33738, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33738
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 33738
US-10-363-483A-33738

Query Match 36.1%; Score 501.2; DB 19; Length 1179;
Best Local Similarity 79.9%; Pred. No. 2.2e-125;
Matches 590; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 1 ATGGGAGCCCTGGAACGGGAGCAGCGCCCGGAGGGGCGCGGAGCCGCGTGGGCC 60
Db 442 ATAAACAACCCCTAAACAGCAACACCGCCCGGAAACCGGAAACCGCGTAACCC 501
QY 61 GGGCTGCGCCCTTGGAGAGCGCGCTGCTCGCCCTTCCCTTGGGCGCGTGTGCGG 120
Db 502 GGGCTACCGCTTAGACGAACCGCGCTACTCGCCCTTCCCTTAAACGCTAATACG 561
QY 121 GTGACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 562 ATAAACCGCTATATACCTATACCTATTCTGCTGGAATAAAGCAACGTAATACCGTA 621
QY 181 ATGCTGATCGGGCTACCGGAGATGCGGACACCAACCACTTCTACTGGGAGCATG 240
Db 622 ATACTAATCGAAGCTTACCGAACAATACGACCAACCACTTATACCTAAACACATA 681
QY 241 GCGGTGTCGACCTACTACTCTGCTCGGGCTGCGGCTTTCGACCTGTACCGCTCTGGGCG 300
Db 682 ACCGTATCGACCTACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741
QY 301 TCGCGCCCTGCGGTGTTGCGGCGCGTGTCTGCGCCCTGTCCCTCTAGTGGGCGAGGCG 360
Db 742 TCGGACCCCTAAATATTCGAACCGCTACTCTACCGCTATCCCTCTACGTAACGAAAC 801
QY 361 TCGACCTAGCCACGCTGTGACATGACCGGCTCAGGCTGAGGCTACCTGCGCATC 420
Db 802 TACACCTAGCCACGCTACTACACATAACCGGCTCAACGCTGCAACGCTTAACCAATC 861
QY 421 TCGCGCCGCTCGGCGCGCTGTTGGTACCGCGCGGCTCGGCGCGCTCATCGCT 480
Db 862 TACCGCGCGCTCGGCGCGCTGTTAATACCGGCGCGCTCGGCGCGCTCATCGT 921
QY 481 GTGCTCTGGGCGGTGGCGCTGCTCTCTGCGCGCTCCCTTCTTCTGTTGGGCGCTGAG 540

Db 922 ATACTCTAAACCGTAACGCTACTCTCTACCGATCCCTTCTTATCTCTAATAACGTCGAA 981
QY 541 CAGGACCCCGGCATCTCCGTAGTCCCGGCTCAATGSCACGCGGATCGCTCTCTCG 600
Db 982 CAAAACCCGACATCTCCGTAATCCGNACTCAATACACGCGGNAATCGCTCTCTCG 1041
QY 601 CCTCTCGCTGCTGCGCGCTCTCTCTGCTGCTGCGGGCGCACCGCGCTCCCGCGCTCG 660
Db 1042 CCTCTCGCTGCTGCGCGCTCTCTAACTCTCGGAAACGCGCACCGCTCCCGCGCTCG 1101
QY 661 GGGCCGAGACCGCGGAGCGCGCGCTGTTACGCGCGGATGCGGCGCGGAGCCCGCG 720
Db 1102 AAACCGGAACCGCGAAACCGCGAGCTATTCAACCGGGAATACCGACCGAACCCCGG 1161
QY 721 CAGCTGGGCGCGCTCGT 738
Db 1162 CAACTAAACGCGCTACGT 1179
RESULT 15
US-10-363-345A-33739
; Sequence 33739, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33739
; LENGTH: 1179
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 33739
US-10-363-345A-33739
Query Match 31.5%; Score 437.2; DB 18; Length 1179;
Best Local Similarity 74.5%; Pred. No. 4.5e-108;
Matches 550; Conservative 0; Mismatches 188; Indels 0; Gaps 0;
QY 1 ATGGGAGCCCTGGAACGGGAGCAGCGCCCGGAGGGGCGCGGAGCCGCGTGGGCC 60
Db 442 ATGGGTAGTCTTGGAAACGGTAGCGATCGTTTCGAGGGGCGCGGAGTCTGCTGGTTC 501
QY 61 GCGCTGCGCGCTTGGAGAGCGCGCTGCTGCGCCCTTTCCTGGGCGCGCTGCTGCGG 120
Db 502 GCGTGTGCTTGGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561
QY 121 GTGACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 562 GTGATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621
QY 181 ATGCTGATCGGGCGCTACCGGAGATGCGGACCAACCACTTCTACTGGGAGCATG 240
Db 622 ATGTTGATCGGGCGCTATCGGGATATCGGATATTAATTAATTTGTAATTTGGGTAGT 681
QY 241 GCGGTGTCGACCTACTCTCTGCTGCGGCTGCGGCTTCGACCTGTACCGCTCTGGGCG 300
Db 682 GTCGTTGTCGATTAATTAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 741
QY 301 TCGGCGCCCTGGGTGTTTCGGCGCGCTGCTCTGCGCCCTGTCCCTCTACGTGGGAGGCG 360
Db 742 TCGGCGTTTGGGTGTTTCGGGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 801
QY 361 TGCACCTAGCCACGCTGCTGCATGACCGGCTCAGGCTGAGGCTACCTGCGCATC 420

Db 802 TGTATTTAGTTACGTTGTTGTAATGATCGGTTTAGCGTCGACGCTTATTGGTTATT 861
QY 421 TGCCGCCCGCTCCGGCCCGCTCTTGGTCAACCGCGCGCGCTCCGGCGCTCATCGCT 480
Db 862 TGTCTGTTCTGTTTCGGGTTCCGGTTTGGTTATTCCGGCTCCGGTTCCGGTTTATCGTT 921
QY 481 GTGCTCTGGGCCGCTGGCGCTGCTCTCTGCGGTCCTTCTTGTTCCTGCTGGGCGTCGAG 540
Db 922 GTGTTTGGGTCGTGGCGTTGTTTGTGCGGTTTGTGCGGTTTGTGCGGTTTGTGCGGTCGAG 981
QY 541 CAGGACCCCGCATCTCCGTAGTCCGGGCTCAATGGCACCGCGCGATCGCCTCCTCG 600
Db 982 TAGGATTTCCGTAATTTCTAGTTTCGGTTTAAATGGTATCGCGCGATCGTTTTCG 1041
QY 601 CCTCTCGCTCTGCGCGCTCTCTGCTCTCGCGGCGCCACCGCCCTCCCGCGCTCG 660
Db 1042 TTTTTCGTTCTGCTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTCGTCG 1101
QY 661 GGGCCCGAGACCGCGAGCCCGCGCTGTTTCAGCCGGAATGCGCGCGAGCCCGCG 720
Db 1102 GGGTTTCGAGATCGCGAGTCGCGGCTGTTTAGTCGGAATGTCGGTCGAGTTTCGCG 1161
QY 721 CAGCTGGGCGCTCGT 738
Db 1162 TAGTTGGCGCGTTGCGT 1179

Search completed: April 11, 2005, 21:00:30
Job time : 819.545 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
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2	230.	16.5	4435	9	AK049671	Mus muscu
3	228.4	16.4	688	7	CO959476	AGENCOURT
C 4	227.8	16.4	640	6	CD618070	CD618070
5	227.8	16.4	640	6	CD618071	CD618071
6	227.8	16.4	1052	9	AY407664	BF603623
7	226.8	16.3	500	2	BF603623	Homo sapi
C 8	225.2	16.2	637	6	CD618076	CD618076
9	219.2	15.8	608	6	BY724644	BY724644
10	218.	15.7	590	2	BF513101	UI-H-BWI-
11	213.2	15.3	969	9	AY407665	AY407665
C 12	203.8	14.7	635	6	CD618069	CD618069
C 13	202.2	14.5	576	6	CD618067	CD618067
C 14	193.2	13.9	643	6	CD618077	CD618077
15	186.4	13.4	843	5	BU553576	BU553576
16	184.6	13.3	635	6	CD618075	CD618075
17	180.6	13.0	634	6	CD618068	CD618068
C 18	174.4	12.5	631	6	CD618073	CD618073
C 19	173.4	12.5	849	5	BU568940	BU568940
C 20	171.	12.3	631	6	CD618074	CD618074
C 21	157.8	11.4	308	9	CES83142	CES83142
22	150.2	10.8	632	6	CD618066	CD618066
C 23	141.2	10.2	504	8	AZ451922	AZ451922
24	134.2	9.7	626	7	CV023556	CV023556

355	Db	CAC	TGTTCCCGCGCGCTGCTGGCGGGCGTCAC	TGCCACCTGTCGTGGCGCTCTTCGTGG	414
152	Qy	TCGGGGTGAGCGGCAACGTGGTGACCGTGATGCTGATCGGGCGCTACCGGGACATGCGGA	211		
415	Db	TGGGCATCTCGGGCAACCTGCTACCATGCTGGTGCTGTCGCGCTTCGCGAGCTGCGCA	474		
212	Qy	CCACCACAACTTGTA	CTGGGCAAGCATGGCCGCTGCCAGCTACTCATCTCTGCTCGGAC	271	
475	Db	CCACCACCAACTCTACCTATCCAGCATGGCCTTCTCCGATCTGCTCATCTTCCTGTGCA	534		
272	Qy	TGCCGTTGACCTGTACCGCCTCTGGCGCTTCGGGCCCTGGGTGTTTGGGGCCGCTGCTCT	331		
535	Db	TGCCGCTGGACCTCGTCGCGCTCTGGCAAGTATCGGCCCTTGAACTTCGCGGACCTGCTCT	594		
332	Qy	GCCGCTGTCCCTCTACGTGGCGAGGCTGCACCTACGCCACGCTGTGTCACATGACCG	391		
595	Db	GCAAACTCTTCAGTTTGTCAGCAGAGCTGCACCTACGCCACGCTCTCAACATCACCG	654		
392	Qy	CGCTCAGCGTCGAGCGCTACCTGGCCATCTGCGGCCGCTCGCGCCCGCGCTTTGGTCA	451		
655	Db	CGCTGAGGTCGAGGCTACTTCGCCATCTGTTCCCGCTCGGGGCAAGTGGTGGTCA	714		
452	Qy	CCGGCGCCGCTCGCGCGCTCATCGCTGTGCTCTGGGCGGTGGCGCTGCTCTCTGGCG	511		
715	Db	CCRAGGGCCGTGTGAAGCTGTGCATCTTGTCATTTGGCCGTGSCCTTCTGCAGCGCG	774		
512	Qy	GTCCCTTCTTGTTCGTGGTGGCGTCGACGAGACCCCGGCA	553		
775	Db	GGCCCATCTTCGTGCTGGTGGCGGTGGAGCAGAGAACGGCA	816		

RESULT	3
COSY9476	
LOCUS	C0959476 688 bp mRNA linear EST 17-AUG-2004
DEFINITION	AGENCOURT 30842629 NIH_MGC_146 Homo sapiens cDNA clone IMAGE:7389798 5' mRNA sequence.

ACCESSION	C0959476	
VERSION	C0959476.1	GI:51324050
KEYWORDS	EST.	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens (human)	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 688)	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Guthrie cDNA Resource Center cDNA Library Preparation: Guthrie cDNA Resource Center cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	

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FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7389798"
/tissue_type="mixed"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_146"
/note="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified from IMAGE clones or
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from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file http://image.llnl.gov/image_rearrayed_plates/IRBF_presv.dat. Note: this is a NIH MGC Library."

ORIGIN

Query Match	16.4%;	Score 228.4;	DB 7;	Length 688;
Best Local Similarity	79.8%;	Pred. No. 3.6e-38;		
Matches 265;	Conservative 0;	Mismatches 67;	Indels 0;	Gaps 0;
QY	1	ATGGGACAGCCCTGGAAACGGCAGCAGCGGCCCGAGGGGGCGCGGGAGCCGCGTGGCCCC	60	
Db	3	ATGGGACAGCCCTGGAAACGGCAGCAGCGGCCCGAGGGGGCGCGGGAGCCGCGTGGCCCC	62	
QY	61	GCCTCTCGCGCTTTGCAACGAGCGCCGCTGCTCGCCCTTTCCCTTGGGGGGCGCTGGTGCCG	120	
Db	63	GCCTCTCGCGCTTTGCAACGAGCGCCGCTGCTCGCCCTTTCCCTTGGGGGGCGCTGGTGCCG	122	
QY	121	GTGACCGCTGTGTGCTGTGCTTTCGTTCGTTCGTTCGGGGTGAGCGGCAACGTGTGTACCGTG	180	
Db	123	GTGACCGCTGTGTGCTGTGCTTTCGTTCGTTCGTTCGGGGTGTCGGGTTCGTGTGTCCGCG	182	
QY	181	ATGCTGATCGGGCGCTACCGGGACATGCGGACACACCAACTGTACCTGGGCACGATG	240	
Db	183	TTGTTGCTCTGGCGCTGTGCGGNGTTGTGAGGCTCTTCCTTCCTTGGCCCTTGGGGCGCGCG	242	
QY	241	GCCTGTTCGGACCTACTCATCTCTGCTCGGCGCTGCCGTTCGACCTGTACCCCTCTTGGCGC	300	
Db	243	TGGGTGCTGNNNGTCTCTCCCGGTTTGCCGCGGGGTGGCGGTGTTCGGCCCTTGGCTC	302	
QY	301	TCGCGGCCCTGGGTGTTCGGGCGCGCTGCTGTG	332	
Db	303	TCGCTGGCNGTGTGTTGTTCCGGTGTGCTTTG	334	

RESULT 4

CD618070	640 bp	mRNA	linear	EST 12-JAN-2004
56030361H1	FLP Homo sapiens cDNA, mRNA sequence.			
CD618070				
CD618070.1	GI:40266335			
EST.				
Source	Homo sapiens (human)			
Organism	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	1 (bases 1 to 640)			
REFERENCE	Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.			
AUTHORS	Circular rapid amplification of cDNA ends for high-throughput			
TITLE	extension cloning of partial genes			
JOURNAL	Genomics 84 (1), 205-210 (2004)			
COMMENT	Contact: Fu GK			
	Incyte Genomics, Inc.			
	3160 Porter Dr., Palo Alto, CA 94304, USA			
	Tel: 6508454102			
	Email: gfu@incyte.com.			
FEATURES	Location/Qualifiers			
source	1..640			

ORIGIN

Query Match 16.4%; Score 227.8; DB 6; Length 640;
Best Local Similarity 68.3%; Pred. No. 4.8e-38;
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;


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153 CGGGGTGAGCGGCAACGTTGACCGTGTATCGGGGCGCTACCGGGACATCGCGAC 212
421 GGGTATCGCTGGCAACCTGCTACCATGCTGGTGGTGTCCGCGAGCTGCGCAC 362
213 CACCACCAACTTGTACTCTGGGCGAGCATGGCGGTGTCGACCTACTCATCTCTGGGCT 272
361 CACCACCAACTTGTACTCTGGGCGAGCATGGCGGTGTCGACCTACTCATCTCTGGGCT 302
273 GCGGTTCAACCTGTACCTCTGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 332
301 GCGGCTGACCTCTGCTGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 242
333 CCGGCTGCGCTGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 392
241 CAAACTCTTCCAACTCTGAGTGGAGCTGACCTACGCGCGCTGCGGCGCTGCGGCGCTGCTGTG 182
393 GCTCAGCGTTCAGCGCTACCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 452
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453 CCGGCGCGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 512
121 CAAAGGGCGGGTGAAGCTGCTCATCTTCTGCTGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 62
513 TCCCTTCTTCTGCTGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 555
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RESULT 5
LOCUS CD618071 640 bp mRNA linear EST 12-JAN-2004
DEFINITION CD618071 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD618071
VERSION CD618071.1 GI:40266336
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 640)
AUTHORS Fu G.K., Wang J.T., Yang J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
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Location/Qualifiers
1..640
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

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ORIGIN
Query Match 16.4%; Score 227.8; DB 6; Length 640;
Best Local Similarity 68.3%; Pred. No. 4.8e-38;
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 93 GCCCTTTCCCTGGGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGT 152
DB 157 GCTCTTCCCGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGT 216
QY 153 CGGGGTGAGCGGCAACGTTGACCGTGTATCGGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGTG 212
DB 217 GGGTATCGTGGCAACCTGCTCACCATGCTGGTGGTGTCCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCGGCG 276

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QY 213 CACCACCAACTTGTACTCTGGGCGAGCATGGCGGTGTCGACCTACTCATCTCTGCTGCGGCT 272
DB 277 CACCACCAACTTGTACTCTGGGCGAGCATGGCGGTGTCGATCTGCTCATCTCTCTCTGCTG 336
QY 273 GCGGTTCAACCTGTACCTCTGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGCGGCGCTGCTGTG 332
DB 337 GCGGCTGAGCGCTGCTGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGCGGCGCTGCTGTG 396
QY 333 CCGGCTGCGCTGCTGCGGCGAGGCGTGCACCTACGCGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 392
DB 397 CAAACTCTTCCAACTCTGAGTGGAGCTGACCTACGCGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 456
QY 393 GCTCAGCGTTCAGCGCTACCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGCGGCGCTGCTGTG 452
DB 457 GCTCAGCGTTCAGCGCTACCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 516
QY 453 CCGGCGCGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 512
DB 517 CAAAGGGCGGGTGAAGCTGCTCATCTTCTGCTGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 576
QY 513 TCCCTTCTTCTGCTGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 555
DB 577 GCCCATCTTCTGCTGCTGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCTGTG 619

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RESULT 6
LOCUS AY407664 1052 bp DNA linear GSS 15-DEC-2003
DEFINITION Homo sapiens GHSR gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY407664
VERSION AY407664.1 GI:39763635
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1052)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1052)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
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Location/Qualifiers
1..1052
/organism="Homo sapiens"
/mol_type="genomic DNA"
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ORIGIN
Query Match 16.4%; Score 227.8; DB 9; Length 1052;
Best Local Similarity 68.3%; Pred. No. 4.9e-38;
Matches 316; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 93 GCCCTTTCCCTGGGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGT 152

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59	GCTCTTCCCGCGCGCTGTGGGGGGCGTCACGCCACTCTCGTGGCACTCTTCGTGGT	118
153	CGGGGTGAGCGGCAACCTGGTGTGACCGTGTGATCTGATCGGGCGCTACTACGGGACATCGGCAC	212
119	GGGTATCGCTGGCAACCTGCTCACCATCTGGTGGTGTGCGCTTCGCGAGCTCGGCAC	178
213	CACCACCAACTTGTACCTGGGACGAGTGGCGGTGCCGACTACTCATCTCTGCTGGGCT	272
179	CACCACCAACCTTACCTGTCCAGATGGCTTCTCCGATCTGCTCATCTTCCTCTGCAT	238
273	GCCCTTCGACCTGTACGCCCTCTGGCGCTCTGGCGCCCTGGGGTTCGGGCGCGCTGCTCTG	332
239	GCCCTTGACCTCGTTGCGCTCTGGCAGTACCGGCGCTTGGAACTTCGGGGAACCTCTCTG	298
333	CGGCGTGTCCCTCTACGTGGGGGAGGGGTGCACCTACGCCACGTGCTGCACATGACCGC	392
299	CAAACTCTTCCAAATTCTGTCAGTGAGAGTGCACCTTACGCCACGGTGTCTCACCATCACAGC	358
393	GCTCAGGTCGAGCGCTACCTGGCCATCTGGCGGCGCTCCGCGCCCGCGCTCTGGTTCAC	452
359	GCTGAGGTCGAGCGCTACTTCGCCATCTGCTTCCCATCTCGGGCACAAGGTGGTGGTCCAC	418
453	CCGGCGCGGCTCCGCGGCTCATCGCTGTGCTCTTGGGCGGCTGGCGGCTCTCTTCGCGGG	512
419	CAAGGGCGGGTGAAGTGGTTCATCTTCGTTCATCTGGGCGGTGGGCTTCTGACGCGCGG	478
513	TCCCTTCTTGTCTCTGTGGGCGGTGAGCAGGACCCCGGCATC	555
479	GCCCATCTTTCGTGTAGTTCGGGGTGGAGCAGAGAAACGGGCACC	521

RESULT 7
BF603623
LOCUS BF603623 500 bp mRNA linear EST 25-APR-2001
DEFINITION 289181 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION	BF603623	
VERSION	BF603623.1	GI:11701421
KEYWORDS	EST.	
SOURCE	Bos taurus	
ORGANISM	Bos taurus (cow)	
	Bos taurus	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
	Bovinae; Bos.	
REFERENCE	1 (bases 1 to 500)	
AUTHORS	Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T.,	
	Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C.,	
	Bennett, G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A.,	
	Chitko-McKown, C. G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,	
	Quackenbush, J. and Keefe, J. W.	
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cdna	
	libraries and construction of a gene index for cattle	
JOURNAL	Genome Res. 11 (4), 626-630 (2001)	
MEDLINE	21180013	
PUBMED	11282978	

COMMENT

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

```

FEATURES
    source
        PCR Primers
        FORWARD: AGGAACAGCTATGACCAT
        BACKWARD: GTTTCCTCAGTCACGACG
        Plate: 49 row: I column: 6
        Seq primer: ATTAGGTGCACTATAG.
        Location/Qualifiers
            1..500
                /organism="Bos taurus"
                /mol_type="mRNA"
                /db_xref="taxon:9913"

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[illegible]

RESULT 8	637 bp	linear	EST 12-JAN-2004
CD618076			
LOCUS	56030461H1	FLP Homo sapiens cDNA, mRNA sequence.	
DEFINITION	CD618076		
ACCESSION	CD618076.1	GI:40266341	
VERSION	EST.		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 637)		
AUTHORS	Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.		
TITLE	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes		
JOURNAL	Genomics 84 (1), 205-210 (2004)		
COMMENT	Contact: Fu GK Incyte Genomics, Inc. 3160 Potter Dr., Palo Alto, CA 94304, USA Tel: 6508454102 Email: gfu@incyte.com.		
FEATURES	Location/Qualifiers		
source	1..637		

FEATURES
SOURCE

PLC I."

ORIGIN

Query Match 15.8%; Score 219.2; DB 6; Length 608;
 Best Local Similarity 70.3%; Pred. No. 3.2e-36;
 Matches 293; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 137 TGTGCTCTTGTGTCGGGTGAGCGGACGAGTGTGACCGTGTGATGTCGCGGCGCT 196
 Db 2 TGGCGCTCTTGTGTCGGGTGAGCGGACGAGTGTGACCGTGTGATGTCGCGGCGCT 61

QY 197 ACCGGACATCGGACACCACTTGTACTGGGAGATGCGCGTGTCCGACCTAC 256
 Db 62 TCCGGAGCTGCGACCACTTGTACTTATCAGATGCGCTTCTCCGATGTC 121

QY 257 TCATCTCTCTGCGGTGCGGTGTGACCTGTATCCGCTCTGCGCTCTGCGGCGCTGGGTGT 316
 Db 122 TCATCTCTCTGCGGTGCGGTGTGACCTGTATCCGCTCTGCGCTCTGCGGCGCTGGGTGT 181

QY 317 TCGGCGCGCTGTCGCGCTGTCCTCTACGTGGGAGGCTGTGACCTACGCGCAGC 376
 Db 182 TCGGCGCGCTGTCGCGCTGTCCTCTACGTGGGAGGCTGTGACCTACGCGCAGC 241

QY 377 TGCTGCATGACCGCGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTG 436
 Db 242 TCCTCACCATCACCAGCGCTGAGCGTGTGAGCGTGTGAGCGTGTGAGCGTGTGAGCGTGT 301

QY 437 CCGCGCTCTTGTGTCACCGCGCGCGCTGCGCGCTCTATCGCTGCTGCTGCGGCGGTGG 496
 Db 302 CCAAGTGTGTCACCAAGGCGGTGTGAGCGTGTGAGCGTGTGAGCGTGTGAGCGTGTG 361

QY 497 CGCTGCTCTGCGCGCTGCTTGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
 Db 362 CTTCTGCGAGCGCGGCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 418

RESULT 10

BF513101

LOCUS

DEFINITION

UI-H-BW1-amm-e-07-0-UI.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone

IMAGE:3070549 3', mRNA sequence.

ACCESSION

BF513101

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Oligo-dt track not found, Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: NCI-CGAP clone distribution
 information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward
 POLYA=No.

FEATURES

Location/Qualifiers

1..590

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3070549"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP Sub7"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not 1; Site 2: Eco RI; NCI CGAP_Sub7
 is a subtracted library derived from NCI CGAP_Sub6. The

NCI CGAP Sub7 library had 12 million recombinants. A
 single-stranded DNA preparation of NCI CGAP_Sub6 was used
 as a tracer in a subtractive hybridization with a driver
 comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM
 3334-3337, 3682-3683, 3798-3803 (IMAGE Clones)
 1322376-1323911, 1456008-1456775, 1500552-1502855);
 NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
 (IMAGE Clones); 1323912-1325831, 1471368-1472903,
 1492104-1493255); NCI CGAP Lu5 pool 1 LLAM 3575-3582,
 3851-3854 (IMAGE Clones); 1414920-1417991,
 1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167,
 3716-3720, 3733-3735 (IMAGE Clones)
 1257096-1258631, 1469064-1470983, 1475592-1476743);
 NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3082-3068
 (IMAGE Clones); 985608-986759, 1101192-1101959,
 1217928-1220615); NCI CGAP_Co10 pool 1 LLAM 2644-2653,
 2871-2872 (IMAGE Clones)
 1057416-1061255, 1144584-1145351). (6% of the driver
 population), plus a pool of 3,840 arrayed clones from
 NCI CGAP_Sub1 (IMAGE Clones 2708616-2710535) and
 NCI CGAP_Sub2 (IMAGE Clones 2710536-2712455) (4% of
 the driver population), plus a pool of 11,136 clones from
 NCI CGAP_Sub3 (IMAGE Clones 2712456-2723591) (10% of
 the driver population), plus a pool of 5,472 clones from
 NCI CGAP_Sub4 (IMAGE Clones 2723592-2729326) (40% of the
 driver population), plus a pool of 4032 clones from
 NCI CGAP_Sub6 (IMAGE Clones 2728969-2733190) (40% of the
 driver population). Subtraction was performed as
 previously described (Bonaldi, Lennon & Soares (1996):
 Normalization and Subtraction: Two Approaches To
 Facilitate Gene Discovery. Genome Research 6, 791-806.
 TAG_SEQ=None found"

ORIGIN

Query Match 15.7%; Score 218; DB 2; Length 590;
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 CGGCGCTGCGAGCGCGCGCTCGGGCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGG 894
 Db 1 CGGCGCTGCGAGCGCGCGCTCGGGCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGG 60

QY 895 GTCTGCTGAGTGGAGCGCGCGTGTTCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 954
 Db 61 GTCTGCTGAGTGGAGCGCGCGTGTTCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

QY 955 GGGACCGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1014
 Db 121 GGGACCGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

QY 1015 GCTCCCTTCTCTATTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTT 1052
 Db 181 GCTCCCTTCTCTATTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTT 218

RESULT 11

AY407665

LOCUS

DEFINITION

Pan troglodytes GHRS gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION

AY407665

VERSION

AY407665.1

KEYWORDS

GI:39763636

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE

1 (bases 1 to 969)

Clark A.G., Glanowski S., Nielson R., Thomas P., Kejarawal A.,
 Todd M.A., Tanenbaum D.M., Civello D.R., Lu F., Murphy B.,
 Perriera S., Wang G., Zheng X.H., White T.J., Sninsky J.J.,
 Adams M.D. and Cargill M.

TITLE

Inferring nonneutral evolution from human-chimp-mouse orthologous

ORIGIN

Query Match 13.9%; Score 193.2; DB 6; Length 643;
Best Local Similarity 67.5%; Pred. No. 1.1e-30;
Matches 301; Conservative 0; Mismatches 143; Indels 2; Gaps 2;

[illegible]

RESULT 15	BU553576	843 bp	mRNA	linear	EST 16-SEP-2002
LOCUS	AGENCOURT_10242213	NTH_MGC_109	Homo sapiens	cdna clone	
DEFINITION	IMAGE:6577973	5' mRNA sequence.			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 843)
 NIH-MGC <http://mgc.ncl.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.

Found through the I.M.A.G.E. Consortium/BLAST at:
<http://image.llnl.gov>
 Plate: LLM2778 row: p column: 05
 High quality sequence stop: 534.
 Location/Qualifiers
 1..843
 /organism="Homo sapiens"
 /mol type="mRNA"

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/db_xref="taxon:9606"  
/clone="IMAGE:6577973"  
/tissue_type="teratocarcinoma, cell line"  
/lab_host="DH10B (phage-resistant)"  
/clone_lib="NIH_MGC_109"  
/note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2:  
XhoI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH_MGC Library."
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ORIGIN

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Query Match      13.4%; Score 186.4; DB 5; Length 843;  
Best Local Similarity 91.0%; Pred. No. 3.2e-29;  
Matches 243; Conservative 0; Mismatches 17; Indels 7; Gaps 4;  
  
Qy 1057 GGTGGTTCTGGCATTATAATTGCTGGTGGCTTCCACCTTCCACGTTGGCAGAACTATTACAT 1116  
Db |||||||  
Qy 534 GGTGGTTCTGGCATTATAATTGCTGGTGGCTTCCACCTTCCACGTTGGCAGAACTATTACAT 593  
Db |||||||  
Qy 1117 AACACGGAAGATTCGCGGATGATGACTTCTCTCAGTACTTTAACATCGTCGCTCTGCA 1176  
Db |||||||  
Qy 594 AACACGGAAGATTCGCGGATGATGACTTCTCTCAGTACTTTAACATCGTCGCTCTGCA 653  
Db |||||||  
Qy 1177 ACTTTTCTATCTGAGCGCATCTATCAACCCCAATCCTCTACACCTC-ATTTCAAAGAAGT 1235  
Db |||||||  
Qy 654 ACTTTTCTATCTGAGCGCATCTATCAACCCCAATCCTCTACACCTCAATTTCAAAGAAGT 713  
Db |||||||  
Qy 1236 AC-AGAGCGCGGCTTTAAA-----CTGCTGCTCGCAGGAAGTCCAGGCGGAG-AGGCT 1289  
Db |||||||  
Qy 714 ACAAGAGCGGCGGCTTTAAACTGCTGCTCGCAAGGGAAGTCCAGGCGGAGGAAGCT 773  
Db |||||||  
Qy 1290 TCCACAGAAGCAGGAGACACTGCGGGG 1316  
Db |||||||  
Qy 774 CCCACAGAAGCAGGAGACACTGCGGGG 800  
Db |||||||
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Search completed: April 11, 2005, 12:57:52
Job time : 5513.89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2005, 12:58:01 ; Search time 64.3333 Seconds
(without alignments)
2320.562 Million cell updates/sec

Title: US-09-719-485-5

Perfect score: 2043

Sequence: 1 MGSPWNGSGPEGAREPWP.....WQNLHKGKRPADDVLLSVL 386

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2043	100.0	386	3	AAY54146 Amino aci
2	2043	100.0	386	4	AAB62653 Short for
3	2043	100.0	386	8	ADN11763 Human mot
4	1581	77.4	412	3	AAY54145 Amino aci
5	1581	77.4	412	4	AAB68478 Amino aci
6	1581	77.4	412	4	AAB62652 Long form
7	1581	77.4	412	5	ABG30936 Human G p
8	1581	77.4	412	5	ABP81993 Human mot
9	1581	77.4	412	8	ADN11761 Human mot
10	1581	77.4	412	8	ADO29697 Human GPC
11	1581	77.4	412	8	ADQ37921 Human G-p
12	1581	77.4	501	4	AAG65822 Human GPR
13	1575	77.1	412	3	AAB02854 Human G p
14	1575	77.1	412	8	ADG86491 Human hgp
15	1575	77.1	412	8	ADG86511 Human orp
16	1575	77.1	412	8	ADP20284 Human GPC
17	1573	77.0	412	5	ABSO9535 Human mot
18	1573	77.0	412	8	ADN12079 Protein #
19	1307	64.0	400	4	AAB68477 Amino aci
20	1149.5	56.3	271	4	AAB68476 Amino aci
21	673.5	33.0	363	3	AAY54147 The puffed
22	673.5	33.0	363	4	AAB68479 Amino aci
23	649	31.8	289	2	AAW19216 Swine gro
24	649	31.8	289	2	AAW19609 Pig growt
25	649	31.8	289	2	AAW19611 Human gro

26	649	31.8	289	6	ABP81828	Abp81828 Human gro
27	644	31.5	289	2	AAW19218	AAW19218 Human gro
28	644	31.5	349	3	AAV69293	AAV69293 A canine
29	643	31.5	366	3	AAV70345	AAV70345 Human G p
30	643	31.5	366	3	AAV90632	AAV90632 Human G p
31	643	31.5	366	4	AAV97376	AAV97376 Rat growt
32	643	31.5	366	4	AAAB62650	AAAB62650 Human G-p
33	643	31.5	366	5	AAAB09534	AAAB09534 Human ghr
34	643	31.5	366	7	ADC22607	ADC22607 Human G p
35	643	31.5	366	7	ADH14080	ADH14080 Human GHS
36	643	31.5	366	8	ADD35398	ADD35398 Human gro
37	643	31.5	366	8	ADN12078	ADN12078 Protein #
38	643	31.5	366	8	ADN11756	ADN11756 Human gro
39	643	31.5	366	8	ADO29025	ADO29025 Human nov
40	643	31.5	366	8	ADQ28857	ADQ28857 Human ghr
41	641	31.4	364	3	AAV54565	AAV54565 A mouse g
42	641	31.4	364	4	AAV97377	AAV97377 Rat growt
43	641	31.4	364	8	ADO29026	ADO29026 Mouse nov
44	639.5	31.3	353	2	AAW19215	AAW19215 Swine gro
45	639.5	31.3	353	2	AAW19608	AAW19608 Pig growt

ALIGNMENTS

RESULT 1
AAY54146

ID AAY54146 standard; protein; 386 AA.

AC AAY54146;

DT 27-MAR-2000 (first entry)

DE Amino acid sequence of the motilin receptor splice variant MTL-R1B.

XX Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;

KW spliced form; MTL-R1A; MTL-R1B; gastric motility disorder;

KW functional defect; neurological disorder; scleroderma; colonoscopy;

KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;

KW infection; stress-related motility disorder; psychogenic disorder;

KW gastroparesis; gastro-oesophageal reflux disease; constipation;

KW chronic idiopathic pseudo obstruction; acute faecal impaction;

KW postoperative ileus; gallstones; infantile colic; diarrhoea;

KW irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;

KW endoscopy; duodenal intubation.

XX Homo sapiens.

XX WO9964436-A1.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-US012773.

XX 12-JUN-1998; 98US-0089098P.

XX (MERI) MERCK & CO INC.

XX Feighner SD, Patchett AA, Tan C, Mckee K, Macneil D, Howard AD;

XX Pong S, Smith RG;

XX WPI; 2000-105868/09.

XX N-PSDB; AAZ45404.

XX Novel receptor protein for screening compounds used in treating irritable
PT bowel syndrome, constipation and other gastric conditions.
PS Claim 5; Fig 5; 44pp; English.
XX The present sequence represents splice variant MTL-R1B of the motilin
CC receptor. The gene encodes a G-protein coupled receptor, and is
CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A
CC (see AAY54145) and MTL-R1B (see AAY54146). MTL-R1A is a functional seven

transmembrane domain form, and MTL-R1B is a truncated five transmembrane domain. The MTL-R1 proteins are used to identify agonists and antagonists which can be used for treating gastric motility disorders, functional defects, disorders secondary to neurological disorders e.g. scleroderma, paraneoplastic syndromes radiation induced dysmotility, diabetes, infections, stress-related motility disorders, psychogenic disorders, chronic gastroparesis, gastro-oesophageal reflux disease, constipation, chronic idiopathic pseudo obstruction, acute faecal impaction, postoperative ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer dyspepsia, non-cardiac chest pain and diarrhoea. They can also be used in the preparation for colonoscopy, endoscopy and duodenal intubation

Query Match 100.0%; Score 2043; DB 3; Length 386;
Best Local Similarity 100.0%; Pred. No. 1e-171;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGSPWNGSDGPGAREPPWPALPCDERRCSPPFLGALVPVTAVCLCLFVVGVSNNVTV 60
1 MGSPWNGSDGPGAREPPWPALPCDERRCSPPFLGALVPVTAVCLCLFVVGVSNNVTV 60
61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYLWRSRPWVFGPPLLCRLSLYVGE 120
61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYLWRSRPWVFGPPLLCRLSLYVGE 120
121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLMAVALLSAGPFLVGVE 180
121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLMAVALLSAGPFLVGVE 180
181 QDPGISVVPGLNGTARIASSPLASPPWLSRAPPSPGPGTAAALFRCRCPSPA 240
181 QDPGISVVPGLNGTARIASSPLASPPWLSRAPPSPGPGTAAALFRCRCPSPA 240
241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRQTVRL 300
241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRQTVRL 300
301 RKWSRSGKDACLOSAPPQTATGLPPLLAQLWAPLPAPFPISIPASTRRGGSGIYNL 360
301 RKWSRSGKDACLOSAPPQTATGLPPLLAQLWAPLPAPFPISIPASTRRGGSGIYNL 360
361 LVALPRWQNLHKGHRFADDDVLLSVL 386
361 LVALPRWQNLHKGHRFADDDVLLSVL 386

RESULT 2
ID AAB62653 standard; protein; 386 AA.
AC AAB62653;
XX AAB62653;
XX 23-JUL-2001 (first entry)
XX Short form of motilin receptor, GPR-38B isoform.
XX zsig33; signal transduction; hormone; enzyme; neural development;
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38B; isoform.
XX Homo sapiens.
XX WO200138955-A2.
XX 31-MAY-2001.
XX 22-NOV-2000; 2000WO-US032074.
XX 22-NOV-1999; 99US-0166765P.
XX

PA (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
PI WPI; 2001-355879/37.
XX N-PSDB; AAF83684.
XX Forming reversible peptide receptor complex for purifying cell and
PT peptides, stimulating signal transduction and modulating hormone
PT secretion, involves contacting a receptor with zsig33 polypeptide.
XX Disclosure; Page 106-109; 111pp; English.
XX The invention relates to a method of forming a reversible peptide-
CC receptor complex that involves providing an immobilized receptor, and
CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
CC is useful for purifying cells, purifying a peptide, stimulating signal
CC transduction in a cell expressing a receptor. It is also useful for
CC modulating secretion of hormones, neural development and/or utilization,
CC gastric contractility, nutrient uptake, secretion of digestive and
CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
CC hormone secretion in a mammal having a disease associated with abnormal
CC levels of growth hormone, such as osteoporosis, bone repair, bone
CC remodeling, low osteoblast levels, cartilage repair and remodeling,
CC skeletal dysplasia, immune suppression, obesity, growth retardation,
CC protein catabolic responses after surgery, cachexia, protein loss,
CC dwarfism, wound healing and ovulation induction. Treating a mammal having
CC a metabolic disorder requiring neurological feedback, such as satiety
CC regulation, glucose absorption and metabolism and neuropathy-associated
CC gastrointestinal disorders, and stimulating glucose-induced insulin
CC release in a mammal. The present sequence represents the short form of
CC motilin receptor, GPR-38B (one of the two isoforms of GPR38 which result
CC from alternative splicing). GPR38 has homology to the human G-protein
CC coupled receptor, GHS-R
XX Sequence 386 AA;
SQ

Query Match 100.0%; Score 2043; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 1e-171;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGSPWNGSDGPGAREPPWPALPCDERRCSPPFLGALVPVTAVCLCLFVVGVSNNVTV 60
1 MGSPWNGSDGPGAREPPWPALPCDERRCSPPFLGALVPVTAVCLCLFVVGVSNNVTV 60
61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYLWRSRPWVFGPPLLCRLSLYVGE 120
61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYLWRSRPWVFGPPLLCRLSLYVGE 120
121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLMAVALLSAGPFLVGVE 180
121 CTYATLLHMTALSVERYLAI CRPLRARVLVTRRRVRLIAVLMAVALLSAGPFLVGVE 180
181 QDPGISVVPGLNGTARIASSPLASPPWLSRAPPSPGPGTAAALFRCRCPSPA 240
181 QDPGISVVPGLNGTARIASSPLASPPWLSRAPPSPGPGTAAALFRCRCPSPA 240
241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRQTVRL 300
241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGHRQTVRL 300
301 RKWSRSGKDACLOSAPPQTATGLPPLLAQLWAPLPAPFPISIPASTRRGGSGIYNL 360
301 RKWSRSGKDACLOSAPPQTATGLPPLLAQLWAPLPAPFPISIPASTRRGGSGIYNL 360
361 LVALPRWQNLHKGHRFADDDVLLSVL 386
361 LVALPRWQNLHKGHRFADDDVLLSVL 386

RESULT 3

CC defects, disorders secondary to neurological disorders e.g. scleroderma,
 CC paraneoplastic syndromes radiation induced dysmotility, diabetes,
 CC infections, stress-related motility disorders, psychogenic disorders,
 CC gastroparesis, gastro-oesophageal reflux disease, constipation, chronic
 CC idiopathic pseudo obstruction, acute faecal impaction, postoperative
 CC ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer
 CC dyspepsion, non-cardiac chest pain and diarrhoea. They can also be used
 CC in the preparation for colonoscopy, endoscopy and duodenal intubation
 XX
 SQ Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 3; Length 412;
 Best Local Similarity 100.0%; Pred. No. 6.6e-131;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSPWNGSDGPEGAREPPWPPALPCDERRCSPFPLGALVPVTAVALCLFLVVGSGNVTV 60
 DB 1 MGSPWNGSDGPEGAREPPWPPALPCDERRCSPFPLGALVPVTAVALCLFLVVGSGNVTV 60
 QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCRLSLYVGE 120
 DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCRLSLYVGE 120
 QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180
 DB 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180
 QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPSPGPGTAETAAALFSRECRPSA 240
 DB 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPSPGPGTAETAAALFSRECRPSA 240
 QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRVL 300
 DB 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRVL 300

RESULT 5
 AAB68478
 ID AAB68478 standard; protein; 412 AA.
 XX
 AC AAB68478;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Amino acid sequence of a human motilin receptor polypeptide.
 XX
 KW Motilin receptor; gastrointestinal disease; gastric motility disorder;
 KW gastroparesis; irritable bowel syndrome; diarrhoea.
 XX
 OS Homo sapiens.
 XX
 PN WO200132710-A1.
 XX
 PD 10-MAY-2001.
 XX
 PF 25-OCT-2000; 2000WO-US029426.
 XX
 PR 29-OCT-1999; 99US-0162264P.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Tan C, McKee K;
 XX
 DR WPI; 2001-343479/36.
 DR N-PSDB; AAF85449.
 XX
 PT Novel polypeptides related to dog and rabbit motilin receptor
 PT polypeptide, comprising unique regions from dog and motilin receptor
 PT amino acid sequence, useful for identifying compounds for treating
 PT diarrhea in humans.
 XX
 PS Disclosure; Page 32-33; 42pp; English.
 XX

CC The present sequence represents a human motilin receptor polypeptide. The
 CC specification describes a unique sequence present in exon 1 of the dog
 CC motilin receptor, which is not present in human or Sphaeroides nephelus
 CC 7587 motilin receptor sequences. The unique nucleic acid sequence is
 CC useful for measuring the ability of a compound to affect motilin receptor
 CC activity. Motilin receptor polynucleotides and polypeptides are used to
 CC identify therapeutic compounds which are useful for treating
 CC gastrointestinal diseases and disorders such as gastric motility
 CC disorders, gastroparesis, irritable bowel syndrome, and diarrhoea
 XX
 SQ Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 4; Length 412;
 Best Local Similarity 100.0%; Pred. No. 6.6e-131;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSPWNGSDGPEGAREPPWPPALPCDERRCSPFPLGALVPVTAVALCLFLVVGSGNVTV 60
 DB 1 MGSPWNGSDGPEGAREPPWPPALPCDERRCSPFPLGALVPVTAVALCLFLVVGSGNVTV 60
 QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCRLSLYVGE 120
 DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPPLCRLSLYVGE 120
 QY 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180
 DB 121 CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180
 QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPSPGPGTAETAAALFSRECRPSA 240
 DB 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPSPGPGTAETAAALFSRECRPSA 240
 QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRVL 300
 DB 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHRTVRVL 300

RESULT 6
 AAB62652
 ID AAB62652 standard; protein; 412 AA.
 XX
 AC AAB62652;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Long form of motilin receptor, GPR-38A isoform.
 XX
 KW zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnerability; immunomodulator; GHS-R;
 KW G-protein coupled receptor; motilin receptor; GPR38; GPR-38A; isoform.
 XX
 OS Homo sapiens.
 XX
 PN WO200138355-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032074.
 XX
 PR 22-NOV-1999; 99US-0166765P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 XX
 DR WPI; 2001-355879/37.
 DR N-PSDB; AAF83683.
 XX
 PT Forming reversible peptide receptor complex for purifying cell and
 PT peptides, stimulating signal transduction and modulating hormone
 PT secretion, involves contacting a receptor with zsig33 polypeptide.
 XX

XX Disclosure; Page 102-104; illpp: English.

XX The invention relates to a method of forming a reversible peptide-receptor complex that involves providing an immobilized receptor, and contacting the receptor with a zsig33 peptide (comprising residues 24-37 of AAB62649), where the receptor binds to the zsig33 peptide. The method is useful for purifying cells, purifying a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, gastric contractility, nutrient uptake, secretion of digestive and pancreatic enzymes and hormones, secretion of insulin-like growth factor I, secretion of non-zsig33 proteins. It is useful for modulating growth hormone secretion in a mammal having a disease associated with abnormal levels of growth hormone, such as osteoporosis, bone repair, bone remodeling, low osteoblast levels, cartilage repair and remodeling, skeletal dysplasia, immune suppression, obesity, growth retardation, protein catabolic responses after surgery, cachexia, protein loss, dwarfism, wound healing and ovulation induction, treating a mammal having a metabolic disorder requiring neurological feedback, such as satiety regulation, glucose absorption and metabolism and neuropathy-associated gastrointestinal disorders, and stimulating glucose-induced insulin release in a mammal. The present sequence represents the long form of motilin receptor, GPR-38A (one of the two isoforms of GPR38 which result from alternative splicing). GPR38 has homology to the human G-protein coupled receptor, GHS-R

XX Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 4; Length 412;
Best Local Similarity 100.0%; Pred. No. 6.6e-131;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAREPPWPALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGVSGNVTV 60
DB 1 MGSPWNGSDGPGAREPPWPALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGVSGNVTV 60

QY 61 MLIGRYDRMTTNTLYLGSMAVSDLLILLGLPFDLYLWRSRPVFGPFLCRLSLYVGE 120
DB 61 MLIGRYDRMTTNTLYLGSMAVSDLLILLGLPFDLYLWRSRPVFGPFLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVE 180
DB 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVE 180

QY 181 QDPGISVVGGLNGTARIASSPLASPPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
DB 181 QDPGISVVGGLNGTARIASSPLASPPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

QY 241 QLGALRVMLVWTVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300
DB 241 QLGALRVMLVWTVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300

RESULT 7
ABG30936
ID ABG30936 standard; protein; 412 AA.
XX AC ABG30936;
XX DT 21-OCT-2002 (first entry)
XX DE Human G protein-coupled receptor 38 (GPR38).
XX KW Human; G protein-coupled receptor 38; receptor; GPR38;
KW Alzheimer's disease; Parkinson's disease; ulcerative colitis;
KW Crohn's disease; Hodgkin's disease; glioblastoma; breast carcinoma;
KW colon carcinoma; lung small cell carcinoma; lung adenocarcinoma;
KW pancreatic small cell carcinoma; pancreatic adenocarcinoma.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers

FT Region 15. .31
FT /note= "Antigenic fragment"
FT 217. .232
FT /note= "Antigenic fragment"
FT 276. .291
FT /note= "Antigenic fragment"
FT 373. .388
FT /note= "Antigenic fragment"
PN WO200257791-A2.
XX 25-JUL-2002.
XX 29-NOV-2001; 2001WO-US045219.
XX 29-NOV-2000; 2000US-0250251P.
XX 30-NOV-2000; 2000US-0250452P.
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX Brown JP, Burmer GC, Roush CL, Kulander BG;
XX WPI; 2002-566812/60.
XX N-FSDB; ABK90132.
XX Assay for detecting Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma or carcinoma, comprises using a binding partner for G protein coupled receptor 38.
XX Disclosure; Fig 2; 112pp; English.
XX The present invention relates to a new assay method that involves contacting a binding partner specific for G protein coupled receptor (GPR) 38 with specific cells. The method of the invention is useful for the detection of an increased risk of Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma, or carcinoma. GPR 38 is used to manufacture a medicament for inhibiting, treating or preventing Alzheimer's disease, Parkinson's disease, ulcerative colitis, Crohn's disease, Hodgkin's disease, glioblastoma, breast carcinoma, colon carcinoma, lung small cell carcinoma, lung adenocarcinoma, pancreatic small cell carcinoma, and pancreatic adenocarcinoma. An agonist or antagonist to GPR 38 are used to manufacture a medicament able to reduce the symptoms of these diseases. Nucleic acids encoding GPR 38 can also be used to treat the diseases. The present amino acid sequence represents the human G protein-coupled receptor 38 (GPR38) of the invention

XX Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 5; Length 412;
Best Local Similarity 100.0%; Pred. No. 6.6e-131;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAREPPWPALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGVSGNVTV 60
DB 1 MGSPWNGSDGPGAREPPWPALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGVSGNVTV 60

QY 61 MLIGRYDRMTTNTLYLGSMAVSDLLILLGLPFDLYLWRSRPVFGPFLCRLSLYVGE 120
DB 61 MLIGRYDRMTTNTLYLGSMAVSDLLILLGLPFDLYLWRSRPVFGPFLCRLSLYVGE 120

QY 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVE 180
DB 121 CTYATLLHMTALSVERVLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVLGVE 180

QY 181 QDPGISVVGGLNGTARIASSPLASPPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240
DB 181 QDPGISVVGGLNGTARIASSPLASPPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

QY 241 QLGALRVMLVWTVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300
DB 241 QLGALRVMLVWTVTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTVRVL 300

RESULT 8
 ABP81993
 ID ABP81993 standard; protein; 412 AA.
 XX
 AC ABP81993;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human motilin receptor GPR38 protein SEQ ID NO:473.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burner GC, Roush CL, Brown JP;
 XX
 DR WPI: 2003-046718/04.
 DR N-PSDB; AB242842.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 PS Disclosure; Fig 1; 533pp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention

SQ Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 6; Length 412;
 Best Local Similarity 100.0%; Pred. No. 6.6e-131; Indels 0; Gaps 0;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSPWNGSDGPEGAREPPWPPALPPCDERRCSPPFLGALVPVTVAVCLCLFVVGVSGNVVTV 60
 DB 1 MGSPWNGSDGPEGAREPPWPPALPPCDERRCSPPFLGALVPVTVAVCLCLFVVGVSGNVVTV 60
 QY 61 MLIGRYDMRTTNYLGSMVAVSDLLILGLPFLYRLWRSRPWVFGFLLCRLSLYVGE 120
 DB 61 MLIGRYDMRTTNYLGSMVAVSDLLILGLPFLYRLWRSRPWVFGFLLCRLSLYVGE 120
 QY 121 CTYATLHMTALSVERVLAICRPURARVLTTRRRVRLIAVLWAVALLSAGFFLFGVGE 180
 DB 121 CTYATLHMTALSVERVLAICRPURARVLTTRRRVRLIAVLWAVALLSAGFFLFGVGE 180
 QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPSPGPTAEAAALFSRECRPSPA 240
 DB 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPSPGPTAEAAALFSRECRPSPA 240
 QY 241 QLGALRVMLWVTYAFPLPFLCISILYGLIGRELWSSRRPLRGPASGRGRHQTVRVL 300
 DB 241 QLGALRVMLWVTYAFPLPFLCISILYGLIGRELWSSRRPLRGPASGRGRHQTVRVL 300
 RESULT 9
 ADN11761
 ID ADN11761 standard; protein; 412 AA.
 XX
 AC ADN11761;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human motilin receptor GPR-38A protein.
 XX
 KW human; zsig33; body weight; body mass; antibody; antagonist;
 KW gastrointestinal; antiinflammatory; antiulcer; vulnerary;
 KW growth hormone secretagogue; GHS-R; peptide-antibody complex;
 KW motilin receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO2004033645-A2.
 XX
 PD 22-APR-2004.
 XX
 PF 06-OCT-2003; 2003WO-US031804.
 XX
 PR 07-OCT-2002; 2002US-0416918P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;
 DR WPI: 2004-340913/31.
 DR N-PSDB; ADN11760.
 XX
 PT Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,
 PT inhibiting signal transduction in a cell expressing a growth hormone
 PT secretagogue receptor, or treating a metabolic disorder.
 XX
 PS Disclosure; Page 95-96; 100pp; English.
 XX
 CC The present invention relates to the use of a zsig33 peptide for forming
 CC a peptide-antibody complex, purifying a peptide, inhibiting signal
 CC transduction in a cell expressing a growth hormone secretagogue receptor
 CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite
 CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a
 CC mammal, or treating a metabolic disorder. The peptide is useful for
 CC forming a peptide-antibody complex, purifying a peptide, inhibiting
 CC signal transduction in a cell expressing a GHS-R, decreasing fat

CC deposition in a mammal, suppressing the appetite of a mammal, inhibiting
CC growth hormone secretion in pituitary cells of a mammal, or treating a
CC metabolic disorder. The zsig33 polypeptides can be used to study
CC proliferation or differentiation in stomach, lung, pituitary,
CC hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,
CC skeletal muscle or pancreas. They are also useful in delivering
CC therapeutic agents. zsig33 polypeptides, agonists and antagonists are
CC also useful for promoting wound healing. The polypeptides, nucleic acids
CC and antibodies are useful for diagnosing, treating or preventing
CC disorders associated with gastric reflux, gastroparesis, modulation of
CC secretion of pituitary hormones, including growth hormone, Crohn's
CC disease, metabolic wasting, gastric ulcers, weight management, or
CC degenerative disease. The present sequence is the human motilin receptor
CC GPR38A protein shown in the exemplification of the invention.
XX
SQ Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 8; Length 412;
Best Local Similarity 100.0%; Pred. No. 6.6e-131;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCCLFVWVGSGNVTV 60
DB 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCCLFVWVGSGNVTV 60

QY 61 MLIGRYRDMRTTNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLVYVGG 120
DB 61 MLIGRYRDMRTTNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLVYVGG 120

QY 121 CTYATLLHMTALSVERYLAICRPLRVLVTRRRVALLAVWALLSAGFFLVGVE 180
DB 121 CTYATLLHMTALSVERYLAICRPLRVLVTRRRVALLAVWALLSAGFFLVGVE 180

QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGSPETAEAAALFSRECRPSA 240
DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGSPETAEAAALFSRECRPSA 240

QY 241 QLGALRVMLVWTVTAYFFLPFLCLSLYGLIGRELWSSRPLRGPAASGRGHRQTVRL 300
DB 241 QLGALRVMLVWTVTAYFFLPFLCLSLYGLIGRELWSSRPLRGPAASGRGHRQTVRL 300

RESULT 10
ADO29697
ID ADO29697 standard; protein; 412 AA.
AC ADO29697;
XX
DT 29-JUL-2004 (first entry)
DE Human GPCR GPR38, SEQ ID NO:799.
XX
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antidiarrhoeic; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW viricide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
receptor.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.
PF
XX 09-SEP-2003; 2002US-0409303P.
XX
PR 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.
PA
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
XX WPI: 2004-390329/36.
DR N-PSDB; ADO30072.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 151; SEQ ID NO 799; 542pp; English.
XX
CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 8; Length 412;
Best Local Similarity 100.0%; Pred. No. 6.6e-131;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCCLFVWVGSGNVTV 60
DB 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTAVCCLFVWVGSGNVTV 60

QY 61 MLIGRYRDMRTTNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLVYVGG 120
DB 61 MLIGRYRDMRTTNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPPLCLSLVYVGG 120

QY 121 CTYATLLHMTALSVERYLAICRPLRVLVTRRRVALLAVWALLSAGFFLVGVE 180
DB 121 CTYATLLHMTALSVERYLAICRPLRVLVTRRRVALLAVWALLSAGFFLVGVE 180

QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGSPETAEAAALFSRECRPSA 240
DB 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGSPETAEAAALFSRECRPSA 240

Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGSETAEAAALFSRECRPSPA 240
 QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTIVRL 300
 Db 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTIVRL 300

RESULT 11
 ADQ37921
 ID ADQ37921 standard; protein; 412 AA.
 XX
 AC ADQ37921;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human G-protein-coupled receptor 38 protein.
 XX
 KW antiparkinsonian; neuroprotective; nootropic; cardiovascular; cardiac;
 KW vasotropic; antiarteriosclerotic; nephrotropic; uropathic;
 KW urology disease; cardiovascular disease;
 KW peripheral nervous system disorder; central nervous system disorder;
 KW G-protein-coupled receptor 38; GPR38; Parkinson's disease;
 KW multiple sclerosis; dementia; myocardial infarction; ischemic disease;
 KW atherosclerosis; renal failure; glomerulopathy; urinary incontinence.
 XX
 OS Homo sapiens.
 XX
 PN .WO2004057328-A2.
 XX
 PD 08-JUL-2004.
 XX
 PF 11-DEC-2003; 2003WO-EP014052.
 XX
 PR 23-DEC-2002; 2002EP-00028753.
 XX
 PA (FARB) BAYER HEALTHCARE AG.
 XX
 PI Golz S, Brueggemeier U, Summer H;
 XX
 DR WPI: 2004-543310/52.
 DR N-PSDB; ADQ37920.
 XX
 PT Screening therapeutic agents for use in treatment of urology diseases and
 PT cardiovascular diseases in a mammal, comprises contacting a test compound
 PT with G-protein-coupled receptor 38, and detecting binding.
 XX
 PS Disclosure; SEQ ID NO 2; 11pp; English.
 XX
 CC The invention relates to a method of screening (M1) for therapeutic
 CC agents useful in the treatment of a disease chosen from urology diseases,
 CC cardiovascular diseases and disorders of the peripheral and central
 CC nervous system in a mammal, comprises contacting a test compound with a G
 CC -protein-coupled receptor 38 (GPR38) polypeptide, and detecting binding
 CC of the test compound to the GPR38 polypeptide. (M1) is useful for
 CC screening therapeutic agents useful in the treatment of a disease chosen
 CC from urology diseases, cardiovascular diseases and disorders of the
 CC peripheral and central nervous system in a mammal, such as Parkinson's
 CC disease, multiple sclerosis, dementia, cardiovascular disorders such as
 CC myocardial infarction, ischemic diseases, atherosclerosis, and urological
 CC disorders such as acute or chronic renal failure, glomerulopathies, and
 CC urinary incontinence. This sequence corresponds to the human G-protein-
 CC coupled receptor 38.
 XX
 SQ Sequence 412 AA;

Query Match 77.4%; Score 1581; DB 8; Length 412;
 Best Local Similarity 100.0%; Pred. No. 6.6e-131;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPWNGSDPGAGAPPALPCDRECSFPFLGALVPVAVCLCLFVGVGNGVNTV 60
 Db 1 MGSPWNGSDPGAGAPPALPCDRECSFPFLGALVPVAVCLCLFVGVGNGVNTV 60

QY 61 MLIGRYDMRTTNNLYLGSMVAVDLLILLGLPFDLYRLWRSPWVFGPLLCRLSLYVGE 120
 Db 61 MLIGRYDMRTTNNLYLGSMVAVDLLILLGLPFDLYRLWRSPWVFGPLLCRLSLYVGE 120
 QY 121 CTYATLLHMTALSVERVLAICRPLRARVLTTRRVRLIAVLWAVALLSAGPFLVLGVE 180
 Db 121 CTYATLLHMTALSVERVLAICRPLRARVLTTRRVRLIAVLWAVALLSAGPFLVLGVE 180
 QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGSETAEAAALFSRECRPSPA 240
 Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGSETAEAAALFSRECRPSPA 240
 QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTIVRL 300
 Db 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAASGRGRHQTIVRL 300

RESULT 12
 AAG65822
 ID AAG65822 standard; protein; 501 AA.
 XX
 AC AAG65822;
 XX
 DT 30-JAN-2002 (first entry)
 XX
 DE Human GPR38 variant GPR38V polypeptide.
 XX
 KW GPR38V; variant; antibacterial; cytostatic; analgesic; antiaesthetic;
 KW anti-Parkinsonian; hypertensive; hypotensive; antidiabetic; osteopathic;
 KW anti-allergic; antimigraine; neuroleptic; nootropic; anticonvulsant;
 KW anti-ulcer; antiemetic; cardiac; vaccine; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2000164836-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006277.
 XX
 PR 01-MAR-2000; 2000US-00516315.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Elshourbagy N, Shabon U;
 XX
 DR WPI: 2001-638956/73.
 DR N-PSDB; AAI65989.
 XX
 PT New human GPR38V polypeptide and polynucleotide, useful for treating e.g.
 PT bacterial, fungal, protozoal and viral infections, cancers or allergies,
 PT as vaccines, and for identifying agonists and antagonists potentially
 PT useful in therapy.
 XX
 PS Claim 1; Page 26; 32pp; English.
 XX
 CC This represents a human GPR38 variant (GPR38V) polypeptide. GPR38V can be
 CC expressed by standard recombinant methodology. The polynucleotides and
 CC polypeptides are used in the treatment of bacterial, fungal, protozoal
 CC and viral infections, infections caused by HIV-1 or HIV-2, pain, cancers,
 CC diabetes, obesity, anorexia, asthma, Parkinson's disease, acute heart
 CC failure, hypertension, urinary retentions, osteoporosis, allergies,
 CC ulcers, migraine, psychotic and neurological disorders, or dyskinesias.
 CC They are also useful for identifying agonists and antagonists that are
 CC potentially useful in therapy, as vaccines to induce immunological
 CC response in a mammal. The polypeptides may also be used as immunogens to
 CC produce antibodies immunospecific for the polypeptides, and to identify
 CC membrane bound or soluble receptors
 XX
 SQ Sequence 501 AA;

Query Match 77.4%; Score 1581; DB 4; Length 501;
 Best Local Similarity 100.0%; Pred. No. 8.3e-131;

Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60

Db 90 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 149

Qy 61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPDLCLSLYVGE 120

Db 150 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPDLCLSLYVGE 209

Qy 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180

Db 210 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 269

Qy 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

Db 270 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 329

Qy 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHQTVRVL 300

Db 330 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHQTVRVL 389

RESULT 13

AAB02854

ID AAB02854 standard; protein; 412 AA.

XX AC AAB02854;

DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor hGPR38 (V297K) protein SEQ ID NO:130.

XX DE Human; G protein coupled receptor; GPCR; transmembrane receptor;

KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US024065.

XX PR 13-OCT-1998; 98US-00170496.

PR 12-NOV-1998; 98US-0108029P.

PR 20-NOV-1998; 98US-0109213P.

PR 27-NOV-1998; 98US-0110060P.

PR 16-FEB-1999; 99US-0120416P.

PR 26-FEB-1999; 99US-0121852P.

PR 12-MAR-1999; 99US-0123944P.

PR 12-MAR-1999; 99US-0123945P.

PR 12-MAR-1999; 99US-0123946P.

PR 12-MAR-1999; 99US-0123948P.

PR 12-MAR-1999; 99US-0123949P.

PR 28-MAY-1999; 99US-0123951P.

PR 28-MAY-1999; 99US-0136436P.

PR 28-MAY-1999; 99US-0136437P.

PR 28-MAY-1999; 99US-0136439P.

PR 28-MAY-1999; 99US-0137127P.

PR 28-MAY-1999; 99US-0137131P.

PR 28-MAY-1999; 99US-0137567P.

PR 27-JUN-1999; 99US-0141448P.

PR 27-AUG-1999; 99US-0151114P.

PR 03-SEP-1999; 99US-0152524P.

PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.

PR 29-SEP-1999; 99US-0156634P.

PR 29-SEP-1999; 99US-0156653P.

PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.

PR 01-OCT-1999; 99US-0157282P.

PR 01-OCT-1999; 99US-0157293P.

PR 01-OCT-1999; 99US-0157294P.

PR 12-OCT-1999; 99US-00416760.

PR 12-OCT-1999; 99US-00417044.

XX (AREN-) ARENA PHARM INC.

XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;

PI Gore M, Liaw CW, Lin I, Lowitz K, White C;

XX N-PSDB; AAA46116.

DR WPI; 2000-317986/27.

XX DR N-PSDB; AAA46116.

XX Non-endogenous, human G protein-coupled receptors for screening receptor,

PT inverse or partial agonists useful as therapeutic agents.

PS Example 2; Page 168-169; 187pp; English.

XX The present invention describes transmembrane receptors, preferably human

CC G protein coupled receptors (GPCR), for which the endogenous ligand is

CC unknown (orphan GPCR receptors). More specifically the present invention

CC relates to non-endogenous, constitutively activated versions of a human

CC GPCR. These non-endogenous human GPCRs can be useful for the direct

CC identification of candidate compounds as receptors agonists, inverse

CC agonists or partial agonists for use as pharmaceutical agents. AAA46017

CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the

CC exemplification of the present invention

XX Sequence 412 AA;

Qy Query Match 77.1%; Score 1575; DB 3; Length 412;

Db Best Local Similarity 99.7%; Pred. No. 2.2e-130;

XX Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60

Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVALCLFVVGSGNVTV 60

Qy 61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPDLCLSLYVGE 120

Db 61 MLIGRYDRMTTNNLYLGSMVSDLLILGLPFDLYRLWRSRPWVFGPDLCLSLYVGE 120

Qy 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180

Db 121 CTYATLLHMTALSVERYLAICRPLARVLVTRRRVRLIAVLWAVALLSAGPFLVGE 180

Qy 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRECRPSA 240

Qy 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHQTVRVL 300

Db 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHQTVRVL 300

RESULT 14

ADG86491

ID ADG86491 standard; protein; 412 AA.

XX AC ADG86491;

XX 11-MAR-2004 (first entry)

XX Human hGPR38 V297K mutant protein.

XX Human; receptor; mutein; endogenous orphan GPCR;

KW G protein-coupled receptor; transmembrane domain 6; mutant.

XX OS Synthetic.

XX OS Homo sapiens.

XX US2003229216-A1.

XX PN

PD 11-DEC-2003.
XX
PF 16-APR-2003; 2003US-00417820.
XX
PR 13-OCT-1998; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123945P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-014448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-00416760.
XX
(CHEN/) CHEN R.
PA (LIAN/) LIAN C W.
PA (LOWI/) LOWITZ K.
PA (CHAL/) CHALMERS D T.
PA (BEHA/) BEHAN D P.
XX
PI Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;
DR WPI; 2004-052038/05.
DR N-PSDB; ADG86490.
XX
XX New cDNA encoding a non-endogenous, constitutively activated version of a
PT human G protein-coupled receptor, useful for identifying receptor,
PT inverse or partial agonists having potential applicability as therapeutic
PT agents.
XX
XX Example 2; SEQ ID NO 130; 110pp; English.
XX
XX The invention relates to a cDNA encoding a non-endogenous, constitutively
CC activated version of a human G protein-coupled receptor comprising HARE-
CC 3 (F313K), HARE-4 (V233K), HARE-5 (A240K), hGPCR14 (L257K), hGPCR27 (C283K),
CC HARE-1 (E232K), HARE-2 (G285K), hPR1 (L239K), hG2A (K232A), hRUP3 (L224K),
CC hRUP5 (A236K), hRUP6 (N267K), hRUP7 (A302K), hCHN4 (V236K), hMC4 (V244K),
CC hCHN3 (S284K), hCHN6 (L355K), hCHN8 (N235K) or hH9 (F236K). Also included are
CC a non-endogenous version of a human G protein-coupled receptor encoded by
CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell
CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively
CC activated version of a human G protein-coupled AT1 receptor comprising
CC the angiotensin II type 1 receptor hAT1 (F239K), hAT1 (N11A),
CC hAT1 (A12K255I3, a domain swap mutant) or hAT1 (A243+). The mutation is of
CC an amino acid 16 residues from the proline in transmembrane domain 6 and
CC is usually to a lysine. The cDNA is useful for identifying candidate
CC compounds as receptor agonists, inverse agonists or partial agonists
CC having potential applicability as therapeutic agents. The present
CC sequence represents a mutated human GPCR.
XX
XX Sequence 412 AA;

Query Match 77.1%; Score 1575; DB 8; Length 412;
Best Local Similarity 99.7%; Pred. No. 2.2e-130; Mismatches 1; Indels 0; Gaps 0;
Matches 299; Conservative 0;
QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPFPGALVPVTAVCLCLFVVGVSNGVTV 60
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPFPGALVPVTAVCLCLFVVGVSNGVTV 60
QY 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120
Db 61 MLIGRYDMRTTNLYLGSMAVSDLLILLGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120
QY 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180
Db 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGV 180
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPSPETAEEAALFSRECRPSA 240
Db 181 QDPGISVVPGLNGTARIASSPPLASSPPLWLSRAPPPSPSPETAEEAALFSRECRPSA 240
QY 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIORELWSSRRPLRGPAASGRERGHRTVRL 300
Db 241 QLGALRVMLWTTAYFFLPFLCLSLYGLIORELWSSRRPLRGPAASGRERGHRTVRL 300
RESULT 15
ADG86511
ID ADG86511 standard; protein; 412 AA.
XX
AC ADG86511;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human orphan GPCR-associated protein #2.
XX
KW Human; endogenous orphan GPCR; G protein-coupled receptor;
KW transmembrane domain 6.
XX
OS Homo sapiens.
XX
PN US2003229216-A1.
XX
PD 11-DEC-2003.
XX
PF 16-APR-2003; 2003US-00417820.
XX
PR 13-OCT-1998; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123945P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-014448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-00416760.

PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
XX
PA (CHEN//) CHEN R.
PA (LIAN//) LIAN C W.
PA (LOWI//) LOWITZ K.
PA (CHAL//) CHALMERS D T.
PA (BEHA//) BEHAN D P.
XX
PI Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;
XX
DR WPI; 2004-052038/05.
XX
XX New cDNA encoding a non-endogenous, constitutively activated version of a
PT human G protein-coupled receptor, useful for identifying receptor,
PT inverse or partial agonists having potential applicability as therapeutic
PT agents.
XX
PS Disclosure; SEQ ID NO 150; 110pp; English.
XX
CC The invention relates to a cDNA encoding a non-endogenous, constitutively
CC activated version of a human G protein-coupled receptor comprising HARE-
CC 3 (F313K), HARE-4 (V233K), HARE-5 (A240K), hGPCR14 (L257K), hGPCR27 (C283K),
CC HARE-1 (E232K), HARE-2 (G285K), hPR1 (L239K), hG2A (K232A), hRUP3 (L224K),
CC hRUP5 (A236K), hRUP6 (N267K), hRUP7 (A302K), hCHN4 (V236K), hMC4 (V244K),
CC hCHN3 (S284K), hCHN6 (L352K), hCHN8 (N235K), or hH9 (F236K). Also included are
CC a non-endogenous version of a human G protein-coupled receptor encoded by
CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell
CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively
CC activated version of a human G protein-coupled AT1 receptor comprising
CC the angiotensin II type 1 receptor hAT1 (F239K), hAT1 (N111A),
CC hAT1 (A2K355IC3, a domain swap mutant) or hAT1 (A243+). The mutation is of
CC an amino acid 16 residues from the proline in transmembrane domain 6 and
CC is usually to a lysine. The cDNA is useful for identifying candidate
CC compounds as receptor agonists, inverse agonists or partial agonists
CC having potential applicability as therapeutic agents. The present
CC sequence is a GPCR-associated protein included in the sequence listing
CC but not mentioned anywhere else in the specification.
XX
SQ Sequence 412 AA;
Query Match 77.1%; Score 1575; DB 8; Length 412;
Best Local Similarity 99.7%; Pred. No. 2.2e-130;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCCLFVVGSGNVVTV 60
Db 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTAVCCLFVVGSGNVVTV 60
QY 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120
Db 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEG 120
QY 121 CYATLLHMTALSVRYLAICRPLRARVLVTRRRYRLAIVLMAVALLSAGPFLFLVGVE 180
Db 121 CYATLLHMTALSVRYLAICRPLRARVLVTRRRYRLAIVLMAVALLSAGPFLFLVGVE 180
QY 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPPETAFAAALFSRECRPSPA 240
Db 181 QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPSPGPPETAFAAALFSRECRPSPA 240
QY 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHROTIVL 300
Db 241 QLGALRVMLWVTYATFFLPFLCLSLYGLIGRELWSSRRPLGPAASGRGRHROTIVL 300

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 11, 2005, 20:05:13 ; Search time 19.8321 Seconds
(without alignments)
1452.926 Million cell updates/sec

Title: US-09-719-485-5
Perfect score: 2043
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1581	77.4	412	US-09-743-742B-8	Sequence 8, Appli
2	649	31.8	289	US-09-077-675A-10	Sequence 10, Appl
3	649	31.8	289	US-09-077-674-10	Sequence 10, Appl
4	644	31.5	349	US-09-762-661A-2	Sequence 2, Appli
5	643	31.5	366	US-09-077-675A-13	Sequence 13, Appl
6	643	31.5	366	US-09-077-674-13	Sequence 13, Appl
7	643	31.5	366	US-09-170-496D-88	Sequence 88, Appl
8	643	31.5	366	US-09-743-742B-7	Sequence 7, Appli
9	643	31.5	366	US-09-762-661A-5	Sequence 5, Appli
10	643	31.5	366	US-09-364-425B-45	Sequence 45, Appl
11	643	31.5	366	US-09-743-475-4	Sequence 4, Appli
12	641	31.4	289	US-09-077-675A-5	Sequence 5, Appli
13	641	31.4	289	US-09-077-674-5	Sequence 5, Appli
14	641	31.4	364	US-09-077-675A-16	Sequence 16, Appl
15	641	31.4	364	US-09-077-674-16	Sequence 16, Appl
16	641	31.4	364	US-09-762-661A-6	Sequence 6, Appli
17	641	31.4	364	US-09-743-475-3	Sequence 3, Appli
18	641	31.4	364	US-09-743-475-5	Sequence 5, Appli
19	641	31.4	366	US-09-762-661A-7	Sequence 7, Appli
20	641	31.4	366	US-09-743-475-6	Sequence 6, Appli
21	639.5	31.3	353	US-09-077-675A-3	Sequence 3, Appli
22	639.5	31.3	353	US-09-077-674-3	Sequence 3, Appli
23	639.5	31.3	361	US-09-077-675A-8	Sequence 8, Appli
24	639.5	31.3	361	US-09-077-674-8	Sequence 8, Appli
25	637	31.2	366	US-09-170-496D-210	Sequence 210, App
26	554	27.1	302	US-09-077-675A-7	Sequence 7, Appli
27	554	27.1	302	US-09-077-674-7	Sequence 7, Appli

28	552	27.0	302	3	US-09-077-675A-2	Sequence 2, Appli
29	552	27.0	302	4	US-09-077-674-2	Sequence 2, Appli
30	454	22.2	271	3	US-09-077-675A-12	Sequence 12, Appl
31	454	22.2	271	4	US-09-077-674-12	Sequence 12, Appl
32	354.5	17.4	403	4	US-09-170-496D-114	Sequence 114, App
33	354.5	17.4	403	4	US-09-743-742B-4	Sequence 4, Appli
34	354.5	17.4	403	4	US-09-743-742B-10	Sequence 10, Appl
35	352.5	17.3	403	4	US-09-170-496D-224	Sequence 224, App
36	335	16.4	412	4	US-09-949-016-10101	Sequence 10101, A
37	335	16.4	415	4	US-09-545-944-2	Sequence 2, Appli
38	335	16.4	415	4	US-09-341-016A-1	Sequence 1, Appli
39	333	16.3	242	4	US-09-684-725-2	Sequence 2, Appli
40	331.5	16.2	405	4	US-09-743-742B-2	Sequence 2, Appli
41	331.5	16.2	405	4	US-09-743-742B-11	Sequence 11, Appli
42	330	16.2	418	4	US-09-743-742B-5	Sequence 5, Appli
43	326.5	16.0	418	4	US-09-826-509-535	Sequence 535, App
44	322	15.8	353	1	US-08-118-270-45	Sequence 45, Appl
45	322	15.8	353	5	PCT-US93-08528-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1

US-09-743-742B-8
; Sequence 8, Application US/09743742B
; Patent No. 6599718
; GENERAL INFORMATION:
; APPLICANT: Liu, Qingyun
; APPLICANT: Howard, Andrew D.
; APPLICANT: McKee, Karen Kudju
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED
; TITLE OF INVENTION: RECEPTORS AND NUCLEIC ACIDS
; FILE REFERENCE: 20217YP
; CURRENT APPLICATION NUMBER: US/09/743,742B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: PCT/US99/15941
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: 60/092,623
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 412
; TYPE: PNT
; ORGANISM: Homo sapiens
US-09-743-742B-8

Query Match		77.4%;	Score 1581;	DB 4;	Length 412;
Best Local Similarity		100.0%;	Pred. No. 3.7e-123;		
Matches 300;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGSPWNGSDGEGAREPWPALPPCDERCCSPFPLGALVPVTAVCLCLFVVGVSQNVTV	60		
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Qy	61	MLICRYDRMRTTNYLIGSMVAVDLLILGLPFDLYRLWRSPWPVFGPLLCRLSLYVGEG	120		
Db	61	MLICRYDRMRTTNYLIGSMVAVDLLILGLPFDLYRLWRSPWPVFGPLLCRLSLYVGEG	120		
Qy	121	CTYATLHMTALSVERYLAI CRPLRVRVLTTRRRVRLIAVLWAVALLSAGPFLVGVGE	180		
Db	121	CTYATLHMTALSVERYLAI CRPLRVRVLTTRRRVRLIAVLWAVALLSAGPFLVGVGE	180		
Qy	181	QDPGISVVGGLNGTARTIASSPLPWLRSRPPSPGPETAAALFSRECRPSPA	240		
Db	181	QDPGISVVGGLNGTARTIASSPLPWLRSRPPSPGPETAAALFSRECRPSPA	240		
Qy	241	QLGALRVMLWTTTAYFFLPFLCLSLTYGLIGRELWSSRRPLRGPAASGRGHRTQTVRL	300		
Db	241	QLGALRVMLWTTTAYFFLPFLCLSLTYGLIGRELWSSRRPLRGPAASGRGHRTQTVRL	300		

APPLICANT: Howard, Andrew D.
APPLICANT: Liberator, Paul A.
APPLICANT: Schaeffer, James M.
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSES: Metck & Co., Inc.
STREET: P.O. Box 2000, 126 B. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,674
FILING DATE: 3-JUN-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19589P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-077-674-13

Query Match 31.5%; Score 643; DB 4; Length 366;
Best Local Similarity 45.1%; Pred. No. 1.8e-45;
Matches 138; Conservative 43; Mismatches 73; Indels 52; Gaps 7;

QY 5 WNGSDGPEGA-----REPPWPALPCD---ERRCSPPFLGALVPTAVCLCLFVVGVSGN 56
DB 2 WNATPSBPFGNLTADLDWDASPGNDSLGDELLQFPAPLLAGVTATCTVALFVVVGIA 61

QY 57 VVTVMILGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLRWRSPWVFGPLLCRLSLY 116
DB 62 LITMLVSRFRELRTTNLYLSSMAFSDLLIFLCPDLVRLWQYRPNWFGDLCKLPQF 121

QY 117 VGEGETATLLHMTALSVERYLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFL 176
DB 122 VSESTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIFVL 181

QY 177 VGVQDPGISVVGINGTARIASSPLASSPPLWLSRAPPPSPGPETAFAALFSRRCR 236
DB 182 VGVHE-----NGT-----DP--W-----DTNECR 199

QY 237 PS--PAQLGALVRLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGHR 294
DB 200 PTEFAVRSGLLTVMWVSSIFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259

QY 295 QTVRVL 300
DB 260 QTVKML 265

RESULT 7
US-09-170-496D-88

Sequence 88, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: NO. 6555339-Endogenous, Constitutively Activated Human G Protein-
FILE REFERENCE: ASEN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patent in version 3.1
SEQ ID NO 88
LENGTH: 366
TYPE: PRT
ORGANISM: Homo sapiens
US-09-170-496D-88

Query Match 31.5%; Score 643; DB 4; Length 366;
Best Local Similarity 45.1%; Pred. No. 1.8e-45;
Matches 138; Conservative 43; Mismatches 73; Indels 52; Gaps 7;

QY 5 WNGSDGPEGA-----REPPWPALPCD---ERRCSPPFLGALVPTAVCLCLFVVGVSGN 56
DB 2 WNATPSBPFGNLTADLDWDASPGNDSLGDELLQFPAPLLAGVTATCTVALFVVVGIA 61

QY 57 VVTVMILGRYDMRTTNLYLGSMAVSDLLILGLPFDLYLRWRSPWVFGPLLCRLSLY 116
DB 62 LITMLVSRFRELRTTNLYLSSMAFSDLLIFLCPDLVRLWQYRPNWFGDLCKLPQF 121

QY 117 VGEGETATLLHMTALSVERYLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFL 176
DB 122 VSESTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIMAVAFCSAGPIFVL 181

QY 177 VGVQDPGISVVGINGTARIASSPLASSPPLWLSRAPPPSPGPETAFAALFSRRCR 236
DB 182 VGVHE-----NGT-----DP--W-----DTNECR 199

QY 237 PS--PAQLGALVRLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGHR 294
DB 200 PTEFAVRSGLLTVMWVSSIFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259

QY 295 QTVRVL 300
DB 260 QTVKML 265

RESULT 8
US-09-743-742B-7
Sequence 7, Application US/09743742B
Patent No. 6599718
GENERAL INFORMATION:
APPLICANT: Liu, Qingyun
APPLICANT: Howard, Andrew D.
APPLICANT: McKee, Karen Kulju
TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED
FILE REFERENCE: 20217YP
CURRENT APPLICATION NUMBER: US/09/743,742B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: PCT/US99/15941
PRIOR FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: 60/092,623
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 366
TYPE: PRT
ORGANISM: Homo sapiens
US-09-743-742B-7

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Query Match      31.5%; Score 643; DB 4; Length 366;
Best Local Similarity 45.1%; Pred. No. 1.8e-45;
Matches 138; Conservative 43; Mismatches 73; Indels 52; Gaps 7;

QY  5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSGN 56
DB  2 WNA TPSEEPGFNLTLADLDWDASPGNDSLGLDQLLQFPAPLAGVTATCVALLFVVGIAGN 61
QY  57 VVTVMILIGRYDRMRTTNLYLGSMAVSDLLILGLPFDLYRLMRSRPWVPFGLCLSLY 116
DB  62 LLTMLVVSFRFELRTTNLYLSSMAFSDLLIFLCMPLDLVRLMQRPNWFGDLCKLQF 121
QY  117 VGEGETYATLLHMTALSVERYLAICRPLARVLTTRRRVRLIAVLWAVALLSAGPFLFL 176
DB  122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFWIAVAFCSAGPIFVL 181
QY  177 VGEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRRCR 236
DB  182 VGVHE-----NGT-----DP--W-----DTNECR 199
QY  237 PS--PAQGLARVMLVMTTAYFFLPFLCLSLYLGILGRELWSSRRPLRGPAAASGRGHR 294
DB  200 PTEFAVRSGLLTVMVWSSIFFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259
QY  295 QTVRVL 300
DB  260 QTVKML 265

RESULT 9
US-09-762-661A-5
; Sequence 5, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Palyana, Oksana C.
; APPLICANT: Smith, Roy G.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1995-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-762-661A-5

Query Match      31.5%; Score 643; DB 4; Length 366;
Best Local Similarity 45.1%; Pred. No. 1.8e-45;
Matches 138; Conservative 43; Mismatches 73; Indels 52; Gaps 7;

QY  5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSGN 56
DB  2 WNA TPSEEPGFNLTLADLDWDASPGNDSLGLDQLLQFPAPLAGVTATCVALLFVVGIAGN 61
QY  57 VVTVMILIGRYDRMRTTNLYLGSMAVSDLLILGLPFDLYRLMRSRPWVPFGLCLSLY 116
DB  62 LLTMLVVSFRFELRTTNLYLSSMAFSDLLIFLCMPLDLVRLMQRPNWFGDLCKLQF 121
QY  117 VGEGETYATLLHMTALSVERYLAICRPLARVLTTRRRVRLIAVLWAVALLSAGPFLFL 176
DB  122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFWIAVAFCSAGPIFVL 181
QY  177 VGEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRRCR 236
DB  182 VGVHE-----NGT-----DP--W-----DTNECR 199
QY  237 PS--PAQGLARVMLVMTTAYFFLPFLCLSLYLGILGRELWSSRRPLRGPAAASGRGHR 294
DB  200 PTEFAVRSGLLTVMVWSSIFFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259
QY  295 QTVRVL 300
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RESULT 11
US-09-743-475-4
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Db 200 PTEFAVRSGLLTVMVWSSIFFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259
QY 295 QTVRVL 300
Db 260 QTVKML 265

RESULT 10
US-09-364-425B-45
; Sequence 45, Application US/09364425B
; Patent No. 6653086
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Chen, Ruoping
; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor
; FILE REFERENCE: Aten0047
; CURRENT APPLICATION NUMBER: US/09/364,425B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/094,879
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/106,300
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/110,906
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-364-425B-45

Query Match      31.5%; Score 643; DB 4; Length 366;
Best Local Similarity 45.1%; Pred. No. 1.8e-45;
Matches 138; Conservative 43; Mismatches 73; Indels 52; Gaps 7;

QY  5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVSGN 56
DB  2 WNA TPSEEPGFNLTLADLDWDASPGNDSLGLDQLLQFPAPLAGVTATCVALLFVVGIAGN 61
QY  57 VVTVMILIGRYDRMRTTNLYLGSMAVSDLLILGLPFDLYRLMRSRPWVPFGLCLSLY 116
DB  62 LLTMLVVSFRFELRTTNLYLSSMAFSDLLIFLCMPLDLVRLMQRPNWFGDLCKLQF 121
QY  117 VGEGETYATLLHMTALSVERYLAICRPLARVLTTRRRVRLIAVLWAVALLSAGPFLFL 176
DB  122 VSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFWIAVAFCSAGPIFVL 181
QY  177 VGEQDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEEAALFSRRCR 236
DB  182 VGVHE-----NGT-----DP--W-----DTNECR 199
QY  237 PS--PAQGLARVMLVMTTAYFFLPFLCLSLYLGILGRELWSSRRPLRGPAAASGRGHR 294
DB  200 PTEFAVRSGLLTVMVWSSIFFFLPVFCLTVLYSLIGRKLWRRRGDAVVGASLRDQNHK 259
QY  295 QTVRVL 300
DB  260 QTVKML 265

RESULT 11
US-09-743-475-4
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Query Match	31.4%;	Score 641;	DB 4;	Length 364;
Best Local Similarity	45.8%;	Pred. No. 2.6e-45;		
Matches 142;	Conservative 41;	Mismatches 65;	Indels 62;	Gaps 10;

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Db	2	WNAT--PSEEPENVTLDWDASPGNDSLFDLPLFPAPLAGVATVCALLVFWGISG	59
QY	56	NVVTVMILIGRYDMRTTNNLYLGSMAVSDDLILGLFPFDLYRLWRSRPWVFGPLLCRLSL	115
Db	60	NLLTMLVVSFRFLRTTNNLYLSSMAFSDLILFLCMLDLVRLWQYEPWFGDLLCKLFQ	119
QY	116	YVGEGCTYATLLHMTALSVERYLAIARPLRARVLVTRRRVALIAVLWAVALLSAGPFLF	175
Db	120	FVSESTCYATVLTITALSVERYFAICPPLRAKVVTGKRVKVLTVLWVAVAFCSAGIFV	179
QY	176	LGVGEODPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPETAEMAAFLSREC	235
Db	180	LGVGEHE-----NGT-----DRPD-----TNEC	197
QY	236	RPS--PAQLGALRVLMLWTTTAYFFLPFLCLISLYGLTIGRLWSSRRPLRGPAAAG---RE	290
Db	198	RATEFAVRSGLLTVMWVSVSVFFFLPVFCITVLYSLIGRLW--RR--RGDAAVGASLRD	253
QY	291	RGRHQTVRVL	300
Db	254	QNHKQTVKML	263

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OM protein - protein search, using sw model

Run on: April 11, 2005, 21:05:05 ; Search time 222.023 Seconds
(without alignments)
577.198 Million cell updates/sec

Title: US-09-719-485-5

Perfect score: 2043

Sequence: 1 MGSPWNGSDGEGAREPPWP.....WNLHLKHGRFADVLLSVL 386

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1581	77.4	412	14	US-10-290-078-15
3	1581	77.4	412	14	US-10-318-661-28
4	1581	77.4	412	14	US-10-206-677-2
5	1575	77.1	412	10	US-09-876-252-130
6	1575	77.1	412	15	US-10-417-820A-130
7	1575	77.1	412	15	US-10-417-820A-150
8	1575	77.1	412	16	US-10-723-955-130
9	649	31.8	289	14	US-10-225-567A-140
10	649	31.8	289	14	US-10-303-204A-10
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12	643	31.5	366	14	US-10-303-204A-13
13	641	31.4	289	14	US-10-303-204A-5

14	641	31.4	364	14	US-10-303-204A-16	Sequence 16, Appl
15	639.5	31.3	353	14	US-10-303-204A-3	Sequence 3, Appl
16	639.5	31.3	361	14	US-10-303-204A-8	Sequence 8, Appl
17	637	31.2	366	14	US-10-251-385-210	Sequence 210, App
18	554	27.1	302	14	US-10-303-204A-7	Sequence 7, Appl
19	552	27.0	302	14	US-10-303-204A-2	Sequence 2, Appl
20	454	22.2	271	14	US-10-303-204A-12	Sequence 12, Appl
21	355.5	17.4	445	15	US-10-240-145-53	Sequence 53, Appl
22	355.5	17.4	445	15	US-10-240-145-139	Sequence 139, App
23	354.5	17.4	403	14	US-10-251-385-114	Sequence 114, App
24	354.5	17.4	403	14	US-10-225-567A-540	Sequence 540, App
25	354.5	17.4	403	14	US-10-290-078-18	Sequence 18, Appl
26	354.5	17.4	403	15	US-10-353-690-10	Sequence 10, Appl
27	354.5	17.4	403	16	US-10-915-157-8	Sequence 8, Appl
28	354.5	17.4	422	16	US-10-367-094-141	Sequence 141, App
29	352.5	17.3	403	14	US-10-251-385-224	Sequence 224, App
30	343	16.8	424	16	US-10-915-157-7	Sequence 7, Appl
31	338	16.5	426	15	US-10-311-671-1	Sequence 1, Appl
32	337.5	16.5	293	16	US-10-770-583-12	Sequence 12, Appl
33	337.5	16.5	296	16	US-10-770-583-10	Sequence 10, Appl
34	335	16.4	402	15	US-10-258-423-4	Sequence 4, Appl
35	335	16.4	412	14	US-10-225-567A-557	Sequence 557, App
36	335	16.4	412	16	US-10-770-583-4	Sequence 4, Appl
37	335	16.4	412	16	US-10-770-583-8	Sequence 8, Appl
38	335	16.4	415	10	US-09-875-076-12	Sequence 12, Appl
39	335	16.4	415	10	US-09-876-252-12	Sequence 12, Appl
40	335	16.4	415	14	US-10-272-983-12	Sequence 12, Appl
41	335	16.4	415	14	US-10-393-807-12	Sequence 12, Appl
42	335	16.4	415	15	US-10-358-423-2	Sequence 2, Appl
43	335	16.4	415	15	US-10-417-820A-12	Sequence 12, Appl
44	335	16.4	415	16	US-10-723-955-12	Sequence 12, Appl
45	335	16.4	415	16	US-10-782-596-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-10-225-567A-473
; Sequence 473, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 473
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-473

Query Match 77.4%; Score 1581; DB 14; Length 412;

Best Local Similarity 100.0%; Pred. No. 8.9e-117;

Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSPWNGSDGEGAREPPWPALPCDERCSPFPGALVPVTAVCLCLFVVGVSNNVTY 60

Db 1 MGSPWNGSDGEGAREPPWPALPCDERCSPFPGALVPVTAVCLCLFVVGVSNNVTY 60

Qy 61 MLIGRYDMRTTTLNLYLGSMVSDLLILGLPFDLYLWRSRPWVFGPLLCRLSLYVGEG 120

Db 61 MLIGRYDMRTTTLNLYLGSMVSDLLILGLPFDLYLWRSRPWVFGPLLCRLSLYVGEG 120

Qy 121 CTYATLHMTALSVERYLAIICRLRARVLVTRRRVRLIAVLWAVALLSAGPFLVGVGE 180


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Db      121  CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGFFFLVGVGE 180
Qy      181  QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPPETAEEAALFSRECRPSPA 240
Db      181  QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPPETAEEAALFSRECRPSPA 240
Qy      241  QLGALRVMLWVTYATFFFLPCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTVRL 300
Db      241  QLGALRVMLWVTYATFFFLPCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTVRL 300

RESULT 2
US-10-290-078-15
; Sequence 15, Application US/102900078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692 or 58874
; FILE REFERENCE: MPI2001-288P1(M)
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-078-15

Query Match      77.4%; Score 1581; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 8.9e-117;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPFLGALVPVTVAVCLCLFVVGVSNGVTV 60
Db      1  MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPFLGALVPVTVAVCLCLFVVGVSNGVTV 60
Qy      61  MLIGRYDRMTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPFLLCRLSLYVGE 120
Db      61  MLIGRYDRMTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPFLLCRLSLYVGE 120
Qy      121  CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGFFFLVGVGE 180
Db      121  CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGFFFLVGVGE 180
Qy      181  QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPPETAEEAALFSRECRPSPA 240
Db      181  QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPPETAEEAALFSRECRPSPA 240
Qy      241  QLGALRVMLWVTYATFFFLPCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTVRL 300
Db      241  QLGALRVMLWVTYATFFFLPCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTVRL 300
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RESULT 3
US-10-318-661-28
; Sequence 28, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superlorigly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
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; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-661-28

Query Match      77.4%; Score 1581; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 8.9e-117;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPFLGALVPVTVAVCLCLFVVGVSNGVTV 60
Db      1  MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPFLGALVPVTVAVCLCLFVVGVSNGVTV 60
Qy      61  MLIGRYDRMTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPFLLCRLSLYVGE 120
Db      61  MLIGRYDRMTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPFLLCRLSLYVGE 120
Qy      121  CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGFFFLVGVGE 180
Db      121  CTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGFFFLVGVGE 180
Qy      181  QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPPETAEEAALFSRECRPSPA 240
Db      181  QDPGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPGPPETAEEAALFSRECRPSPA 240
Qy      241  QLGALRVMLWVTYATFFFLPCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTVRL 300
Db      241  QLGALRVMLWVTYATFFFLPCLSLYGLIGRELWSSRRPLRGPAASGRERGHRTVRL 300
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RESULT 4
US-10-206-677-2
; Sequence 2, Application US/10206677
; Publication No. US20030186336A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences, Inc.
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; APPLICANT: Kullander, Bruce G.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO
; TITLE OF INVENTION: GPCR 38, A G PROTEIN-COUPLED RECEPTOR (GPCR)
; FILE REFERENCE: 1920-1-8
; CURRENT APPLICATION NUMBER: US/10/206,677
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/250,251
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,452
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-206-677-2

Query Match      77.4%; Score 1581; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 8.9e-117;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPFLGALVPVTVAVCLCLFVVGVSNGVTV 60
Db      1  MGSPWNGSDGPEGAREPPWPALPPCDERRCSPPFLGALVPVTVAVCLCLFVVGVSNGVTV 60
Qy      61  MLIGRYDRMTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPFLLCRLSLYVGE 120
Db      61  MLIGRYDRMTTNNLYLGSMVSDLLILLGLPFDLYRLWRSRPWVFGPFLLCRLSLYVGE 120
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QY 121 CTYATLLHMTALSVRYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE 180
DB 121 CTYATLLHMTALSVRYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE 180
QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPTAAALFSRECRPSA 240
DB 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPTAAALFSRECRPSA 240
QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRERGHRTQVRL 300
DB 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRERGHRTQVRL 300

RESULT 5

US-09-876-252-130
; Sequence 130, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29

; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 130
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-130
Query Match 77.1%; Score 1575; DB 10; Length 412;
Best Local Similarity 99.7%; Pred. No. 2.7e-116;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPPLGALVPVTVAVCLCLFVVGVSNGVTV 60
DB 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPPLGALVPVTVAVCLCLFVVGVSNGVTV 60
QY 61 MLIGRYDMRTTNLYLGSMASVSDLLILLGLPFDLYRLWRSRPWVFGPLCLSLYVGE 120
DB 61 MLIGRYDMRTTNLYLGSMASVSDLLILLGLPFDLYRLWRSRPWVFGPLCLSLYVGE 120
QY 121 CTYATLLHMTALSVRYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE 180
DB 121 CTYATLLHMTALSVRYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLFLVGVE 180
QY 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPTAAALFSRECRPSA 240
DB 181 QDPGISVVPGLNGTARIASSPPLWLSRAPPPSPGPTAAALFSRECRPSA 240
QY 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRERGHRTQVRL 300
DB 241 QLGALRVMLWVTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRERGHRTQVRL 300

RESULT 6

US-10-417-820A-130
; Sequence 130, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: 7 US28 CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416

/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,951
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,951
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 155
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 130
/ LENGTH: 412
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-417-820A-130

Query Match 77.1%; Score 1575; DB 15; Length 412;
Best Local Similarity 99.7%; Pred. No. 2.7e-116;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGVSNGVTV 60
DB 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGVSNGVTV 60

QY 61 MLIGRYDMRTTNNLYGSMAYSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120
DB 61 MLIGRYDMRTTNNLYGSMAYSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120

QY 121 CYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGE 180
DB 121 CYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGE 180

QY 181 QDPGISVVGNGTARIASSPLASPPPLWLSRAPPSPGPETAEEAALFSRECRPSA 240
DB 181 QDPGISVVGNGTARIASSPLASPPPLWLSRAPPSPGPETAEEAALFSRECRPSA 240

QY 241 QLGALRVMLWVTYAFFLPFLCLSLYGLIGELWSSRRPLRGPAASGRGRHQTVRVL 300
DB 241 QLGALRVMLWVTYAFFLPFLCLSLYGLIGELWSSRRPLRGPAASGRGRHQTVRVL 300

RESULT 7
US-10-417-820A-150
/ Sequence 150, Application US/10417820A
/ Publication No. US20030229216A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lowitz, Kevin
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Behan, Dominic P.
/ TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: 7:US28.CON
/ CURRENT APPLICATION NUMBER: US/10/417,820A
/ CURRENT FILING DATE: 2003-04-16
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213

/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,951
/ PRIOR FILING DATE: 1999-03-12
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 155
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 150
/ LENGTH: 412
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-417-820A-150

Query Match 77.1%; Score 1575; DB 15; Length 412;
Best Local Similarity 99.7%; Pred. No. 2.7e-116;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGVSNGVTV 60
DB 1 MGSPWNGSDGPEGAREPPWALPPCDERRCSPFPLGALVPVTVAVCLCLFVVGVSNGVTV 60

QY 61 MLIGRYDMRTTNNLYGSMAYSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120
DB 61 MLIGRYDMRTTNNLYGSMAYSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120

QY 121 CYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGE 180
DB 121 CYATLLHMTALSVERYLAI CRPLARVLVTRRRVRLIAVLWAVALLSAGPFLFLVGE 180

QY 181 QDPGISVVGNGTARIASSPLASPPPLWLSRAPPSPGPETAEEAALFSRECRPSA 240
DB 181 QDPGISVVGNGTARIASSPLASPPPLWLSRAPPSPGPETAEEAALFSRECRPSA 240

QY 241 QLGALRVMLWVTYAFFLPFLCLSLYGLIGELWSSRRPLRGPAASGRGRHQTVRVL 300
DB 241 QLGALRVMLWVTYAFFLPFLCLSLYGLIGELWSSRRPLRGPAASGRGRHQTVRVL 300

RESULT 8
US-10-723-955-130
/ Sequence 130, Application US/10723955
/ Publication No. US20040110238A1
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lehman-Bruinsma, Karin
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Gore, Martin
/ APPLICANT: White, Carol
/ TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: 7:US29.CON
/ CURRENT APPLICATION NUMBER: US/10/723,955
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: 10/417,820
/ PRIOR FILING DATE: 2003-4-16
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16

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; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-955-130

Query Match      77.1%; Score 1575; DB 16; Length 412;
Best Local Similarity 99.7%; Pred. No. 2.7e-116;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSPWNGSDGPGAGPEPKPAPPCDERRCSPPFLGALVPVTAVCLCLFVVGVSNGNVTV 60
DB 1 MGSPWNGSDGPGAGPEPKPAPPCDERRCSPPFLGALVPVTAVCLCLFVVGVSNGNVTV 60
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DB 61 MLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLYVGE 120
QY 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLVGE 180
DB 121 CYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFLVGE 180
QY 181 QPGLSVVPGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRSPA 240
DB 181 QPGLSVVPGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECRSPA 240
QY 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGHRQTVRL 300
DB 241 QLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGHRQTVRL 300

RESULT 9
US-10-225-567A-140
; Sequence 140, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-140

Query Match      31.8%; Score 649; DB 14; Length 289;
Best Local Similarity 43.2%; Pred. No. 3.1e-43;
Matches 145; Conservative 46; Mismatches 87; Indels 59; Gaps 8;

QY 5 WNGSDGPEGA-----REPPWPALPPCD----ERRCSPPFLGALVPVTAVCLCLFVVGVSNGN 56
DB 5 WNGSDGPEGA-----REPPWPALPPCD----ERRCSPPFLGALVPVTAVCLCLFVVGVSNGN 56
QY 57 VVTWMLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLY 116
DB 57 VVTWMLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLY 116
QY 117 VGECTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFL 176
DB 117 VGECTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFL 176
QY 176 VSECTYATVLTITALSVERYFAICFPPLRAKVVTKGRVKLVIFVIMAVAFCSAGPIFVL 181
DB 176 VSECTYATVLTITALSVERYFAICFPPLRAKVVTKGRVKLVIFVIMAVAFCSAGPIFVL 181
QY 181 VGEQDPGIVSVVPGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECR 236
DB 181 VGEQDPGIVSVVPGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECR 236
```

```
DB 2 WNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVATATCVALFVVGVIAGN 61
QY 57 VVTWMLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLY 116
DB 57 VVTWMLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLY 116
QY 117 VGECTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFL 176
DB 117 VGECTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFL 176
QY 176 VSECTYATVLTITALSVERYFAICFPPLRAKVVTKGRVKLVIFVIMAVAFCSAGPIFVL 181
DB 176 VSECTYATVLTITALSVERYFAICFPPLRAKVVTKGRVKLVIFVIMAVAFCSAGPIFVL 181
QY 181 VGEQDPGIVSVVPGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECR 236
DB 181 VGEQDPGIVSVVPGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECR 236
QY 237 PS--PAQLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGHR 294
DB 237 PS--PAQLGALRVMLVWTTAYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAASGRGHR 294
QY 294 PTEFAVRSGLLTVMVWVSSIFFFLPVFCLTVLYSLIGRKLWRRRRGDAVVGASLRDQNHK 259
DB 294 PTEFAVRSGLLTVMVWVSSIFFFLPVFCLTVLYSLIGRKLWRRRRGDAVVGASLRDQNHK 259
QY 295 QTVRVLRKWSRRGSKDACLOQSAAPPQTAOTLGLPLLL 330
DB 295 QTVRVLRKWSRRGSKDACLOQSAAPPQTAOTLGLPLLL 330
QY 330 QTVKML-----GGQRALRLSLAGPILSLCLLPSL 289
DB 330 QTVKML-----GGQRALRLSLAGPILSLCLLPSL 289

RESULT 10
US-10-303-204A-10
; Sequence 10, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 289
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-303-204A-10

Query Match      31.8%; Score 649; DB 14; Length 289;
Best Local Similarity 43.2%; Pred. No. 3.1e-43;
Matches 145; Conservative 46; Mismatches 87; Indels 59; Gaps 8;

QY 5 WNGSDGPEGA-----REPPWPALPPCD----ERRCSPPFLGALVPVTAVCLCLFVVGVSNGN 56
DB 5 WNGSDGPEGA-----REPPWPALPPCD----ERRCSPPFLGALVPVTAVCLCLFVVGVSNGN 56
QY 57 VVTWMLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLY 116
DB 57 VVTWMLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDLYRLWRSRPWVFGPLLCRLSLY 116
QY 117 VGECTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFL 176
DB 117 VGECTYATLLHMTALSVERYLAICRPLRARVLVTRRRVRALIAVLWAVALLSAGPFL 176
QY 176 VSECTYATVLTITALSVERYFAICFPPLRAKVVTKGRVKLVIFVIMAVAFCSAGPIFVL 181
DB 176 VSECTYATVLTITALSVERYFAICFPPLRAKVVTKGRVKLVIFVIMAVAFCSAGPIFVL 181
QY 181 VGEQDPGIVSVVPGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECR 236
DB 181 VGEQDPGIVSVVPGINGTARIASSPLASSPPLWLSRAPPPSPGPTAEAAALFSRECR 236
```



```
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 289
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-5

Query Match      31.4%; Score 641; DB 14; Length 289;
Best Local Similarity 43.3%; Pred. No. 1.3e-42;
Matches 142; Conservative 45; Mismatches 77; Indels 64; Gaps 9;

Qy  5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPPPLGALVPVTAVCLCLFVVGSGN 56
Db  2 WNATPSEBPGPNLTLPDLGWDAPPENDSLVBELLPLFPPTLLAGVTATCTVALFVVGIG 61

Qy  57 VVTVMILGRYDRMTTNNLYLGSMAVSDLLILGLPFDPDLRLWRSRPMVFGPLLCRLSLY 116
Db  62 LLTLMVSRFRMRTTNNLYLSSMAFSELLFLCMLPDLRLWQYRPMWFGDLCCLFQ 121

Qy  117 VGEGETATLHMTALSVERYLAICRPLRARVLVTRRRVRLAIVLWAVALLSAGPFLF 176
Db  122 VSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVILVWAVAFCSAGPIFVL 181

Qy  177 VGVODPGISVVGPLNGTARIASSPLASSPPLWLSRAPPPSPGPETAABAAALFSRRCR 236
Db  182 VGVVHE-----NGT-----DPRD-----TNECR 199

Qy  237 PS--PAQLGALRMLVWTTAYFFLPCLCLSYLGLIGRELWSSRRPLRGPASG---RER 291
Db  200 ATEFAVRSGLLTVMVWSSVFFFLPVFCLTVLYSLIGRKLW---RRKRGEAAVGSUKDQ 256

Qy  292 GHRQTVRLKWSRRGSKDACIQSAPPG 319
Db  257 NHKQTVKML-----GGSQCALELSLPG 278

RESULT 14
US-10-303-204A-16
; Sequence 16, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 364
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-3

Query Match      31.3%; Score 639.5; DB 14; Length 353;
Best Local Similarity 47.2%; Pred. No. 2.2e-42;
Matches 137; Conservative 39; Mismatches 61; Indels 53; Gaps 7;

Qy  19 WPALPPCD---ERRCSPPPLGALVPVTAVCLCLFVVGSGNVVTVMLIGRYDRMTTNNL 75
Db  8 WDAPPENDSLVBELLPLFPPTLLAGVTATCTVALFVVGIGLNTMLVVRFRMRTTNNL 67

; ORGANISM: rattus norvegicus
US-10-303-204A-16

Query Match      31.4%; Score 641; DB 14; Length 364;
Best Local Similarity 45.8%; Pred. No. 1.7e-42;
Matches 142; Conservative 41; Mismatches 65; Indels 62; Gaps 10;

Qy  5 WNGSDGPEGAREP-----PMPALPPCD---ERRCSPPPLGALVPVTAVCLCLFVVGSG 55
Db  2 WNAT--PSEDEPNVTLDDMDASFGNDSLDPDELLPLFPAPLLAGVTATCTVALFVVGISG 59

Qy  56 NVTVMLIGRYDRMTTNNLYLGSMAVSDLLILGLPFDPDLRLWRSRPMVFGPLLCRLSL 115
Db  60 NLTLMLVSRFRMRTTNNLYLSSMAFSDLLIFCMLPDLRLWQYRPMWFGDLCCLFQ 119

Qy  116 VVGCGCTATLHMTALSVERYLAICRPLRARVLVTRRRVRLAIVLWAVALLSAGPFLF 175
Db  120 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVILVWAVAFCSAGPIFV 179

Qy  176 LVGVEODPGISVVGPLNGTARIASSPLASSPPLWLSRAPPPSPGPETAABAAALFSRRCR 235
Db  180 LVGVHE-----NGT-----DPRD-----TNEC 197

Qy  236 RPS--PAQLGALRMLVWTTAYFFLPCLCLSYLGLIGRELWSSRRPLRGPASG---RE 290
Db  198 RATEFAVRSGLLTVMVWSSVFFFLPVFCLTVLYSLIGRKLW---RR--RGDAAVGASLRD 253

Qy  291 RGHQTVRVL 300
Db  254 QNHQTVKML 263

RESULT 15
US-10-303-204A-3
; Sequence 3, Application US/10303204A
; Publication No. US20030166144A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-303-204A-3
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QY 76 YLGSMVSDLLILLGLPFDLYRLWRSRPWVGFELLCRLSLYVGEQCTYATLLHMTALSVE 135
Db 76 YLGSMVSDLLILLGLPFDLYRLWRSRPWVGFELLCRLSLYVGEQCTYATLLHMTALSVE 135
QY 68 YLSSMAFSDLLIFLCMPLDLFRLWQYRPWNLGNLLCKLFQVSESCYATVLTITALSVE 127
Db 68 YLSSMAFSDLLIFLCMPLDLFRLWQYRPWNLGNLLCKLFQVSESCYATVLTITALSVE 127
QY 136 RYLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFLYGVQODPGISVVPGLNGTA 195
Db 136 RYLAICRPLRARVLTTRRRVRALIAVLWAVALLSAGPFLFLYGVQODPGISVVPGLNGTA 195
QY 128 RYPAICFPLRAKVVVTKGRVKLVILVIMAVAFCSAGPIFVLVGVVHD-----NGT- 177
Db 128 RYPAICFPLRAKVVVTKGRVKLVILVIMAVAFCSAGPIFVLVGVVHD-----NGT- 177
QY 196 RIASSPLASSPPLWLSRAPPPGPPGPETAEEAALFSRECRPS--PAQLGALRVMLWVTT 253
Db 196 RIASSPLASSPPLWLSRAPPPGPPGPETAEEAALFSRECRPS--PAQLGALRVMLWVTT 253
QY 178 -----DPRD-----TNECRATEFAVRSGLLTVVWVSS 205
Db 178 -----DPRD-----TNECRATEFAVRSGLLTVVWVSS 205
QY 254 AYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAG---FERGHRQTVRYL 300
Db 254 AYFFLPFLCLSLYGLIGRELWSSRRPLRGPAAG---FERGHRQTVRYL 300
QY 206 VFFFLVFLVCLTVLYSLIGRKLW---RRKGEAAVGSRLRDQNHKQIVKWL 252
Db 206 VFFFLVFLVCLTVLYSLIGRKLW---RRKGEAAVGSRLRDQNHKQIVKWL 252
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Search completed: April 11, 2005, 21:21:25
Job time : 223.023 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2005, 19:24:50 ; Search time 16.4461 Seconds
(without alignments)
2258.264 Million cell updates/sec

Title: US-09-719-485-5
Perfect score: 2043
Sequence: 1 MGSPWNGSDGPEGAREPPWP.....WQNLHLKHGRFADVDLLSVL 386

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	343	16.8	424	2 JH0164	neurotensin recept
2	330	16.2	418	2 S29506	neurotensin recept
3	316	15.5	477	2 JC7913	capa receptor (CG1
4	285.5	14.0	418	2 A88013	protein K10B4.4 [i
5	268.5	13.1	416	2 S68822	neurotensin recept
6	261	12.8	595	2 JC8012	G protein-coupled
7	255.5	12.5	378	2 T15816	hypothetical prote
8	253.5	12.4	367	2 JC2421	opioid receptor ho
9	253.5	12.4	367	2 I49022	kappa opioid recep
10	253.5	12.4	367	2 I56520	G protein-coupled
11	253.5	12.4	370	2 J43087	orphan opioid rece
12	252.5	12.4	658	2 JC8011	G protein-coupled
13	250.5	12.3	363	2 I57940	somatostatin recep
14	249.5	12.2	452	2 JC2459	gastrin/cholecysto
15	249.5	12.2	452	2 A46195	cholecystokinin B
16	248.5	12.2	418	2 A46226	somatostatin recep
17	247	12.1	453	2 S32817	gastrin receptor -
18	245.5	12.0	363	2 I57955	somatostatin recep
19	245.5	12.0	364	2 JN0763	somatostatin recep
20	243	11.9	359	2 JC5277	G protein-coupled
21	241.5	11.8	477	1 QRRUB1	beta-1-adrenergic
22	240	11.7	450	2 JQ1614	gastrin receptor -
23	239	11.7	352	2 JQ0296	thyrotropin releas
24	237.5	11.6	447	2 A47430	gastrin/cholecysto
25	237.5	11.6	519	2 S17783	tachykinin recepto
26	234.5	11.5	514	2 D56849	dopamine receptor-
27	233.5	11.4	480	2 I53053	beta 1 adrenergic
28	232.5	11.4	379	2 JC6178	serotonin receptor
29	232.5	11.4	450	2 I49481	alpha-2 adrenergic

30	232	11.4	380	2 A55259	kappa opioid recep
31	230	11.3	477	2 T25846	hypothetical prote
32	229.5	11.2	466	2 S36794	beta-1-adrenergic
33	229	11.2	427	2 S50150	gastric CCK-A rece
34	228.5	11.2	387	2 JC5949	galanin receptor 2
35	228	11.2	437	2 I57942	5-hydroxytryptamin
36	228	11.2	450	2 B40392	alpha-2-adrenergic
37	227.5	11.1	428	2 S30508	probable G protein
38	227	11.1	380	2 JC2338	kappa opioid recep
39	227	11.1	418	2 G02953	beta-3-adrenergic
40	226	11.1	398	2 JN0708	thyrotropin-releas
41	225	11.0	444	2 A42685	cholecystokinin re
42	224.5	11.0	411	2 I56444	thyrotropin-relea
43	224.5	11.0	412	2 S23436	thyroliberin recep
44	224.5	11.0	428	2 A44021	somatostatin recep
45	224	11.0	483	2 A25896	beta-adrenergic re

ALIGNMENTS

RESULT 1
JH0164
neurotensin receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JH0164
R:Tanaka, K.; Masu, M.; Nakanishi, S.
Neuron 4, 847-854, 1990
A:Title: Structure and functional expression of the cloned rat neurotensin receptor.
A:Reference number: JH0164; MUID:90297956; PMID:1694443
A:Accession: JH0164
A:Molecule type: mRNA
A:Residues: 1-424 <TAN>
A:Cross-references: UNIPROT:P20789
C:Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor. The
ter (neurotransmitter) in the brain and as a hormone) cellular mediator in peripheral tiss
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:65-87/Domain: transmembrane #status predicted <TM1>
F:97-121/Domain: transmembrane #status predicted <TM2>
F:144-165/Domain: transmembrane #status predicted <TM3>
F:189-210/Domain: transmembrane #status predicted <TM4>
F:236-260/Domain: transmembrane #status predicted <TM5>
F:309-330/Domain: transmembrane #status predicted <TM6>
F:348-372/Domain: transmembrane #status predicted <TM7>
F:4,38,42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	16.8%	Score	343	DB	2	Length	424
Best Local Similarity	33.9%	Pred. NO.	9.3e-19				
Matches	82	Conservative	41	Mismatches	71	Indels	48
Gaps	6						
QY	39	VPVTVAVCLFVGVGNGVNVTVMLIGR	---	YRDMETTNLVILGSMVAVSDLLI	-	LLGLPFD	94
DB	65	VLVTAIYALFVGVGVGNSVTAFTLARKKSIQSLQSTVHYHLGSLALSDLLILLAMPVE	124				
QY	95	LYR-LWRSRPVVFGLLCRLSLYVGEGETYATLHMTALSVERYLAICRFLARVLVTRR	153				
DB	125	LYNFIWVHHPAFGDAGCGYFFLEDCTATALNVASLSVERYLAICHPFKAKTLMRSR	184				
QY	154	RVRALIAVLWAVALLSAGPFPLVGVGEQDPGLSVVGVGLNGTARIASSPLASSPPLWLSRA	213				
DB	185	RTKKFISAIWLASALLAIPMLFTMGLQNRSGDTHPG	---	GLVCTPIVD	---	---	231
QY	214	PPPPSPSPFETAAALFSPRCRSPAQGLGALRVMLWTTAYFFL	-	PFCLSLYGLIGR	272		
DB	232	---	---	---	---	---	---
QY	273	EL	274				
DB	263	KL	264				

A:Reference number: S68822; MUID:96228041; PMID:8647296

A:Accession: S68822

A:Molecule type: mRNA

A:Residues: 1-416 <CHA>

A:Cross-references: UNIPROT:Q63384; GB:X97121; NID:g1483579; PIDN:CAA65787.1; PID:g14835

A:Experimental source: hypothalamus

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:33-58/Domain: transmembrane #status predicted <TM1>

F:70-91/Domain: transmembrane #status predicted <TM2>

F:110-131/Domain: transmembrane #status predicted <TM3>

F:158-175/Domain: transmembrane #status predicted <TM4>

F:204-230/Domain: transmembrane #status predicted <TM5>

F:296-315/Domain: transmembrane #status predicted <TM6>

F:335-361/Domain: transmembrane #status predicted <TM7>

Query Match 13.1%; Score 268.5; DB 2; Length 416;

Best Local Similarity 37.9%; Pred. No. 4.3e-13;

Matches 66; Conservative 33; Mismatches 66; Indels 9; Gaps 4;

Qy 18 PWPALP-----PCDERCSPFLGALVPVAVCLCLFVVGSGNVVTMLIGRYDMRT 71

Db 6 PWPSPSPSAGLSLEARLGVDTLWAKVLTALYSLIFAFGTAGNALSVHVLKARAGR 65

Qy 72 -TTNLYLGMAVSDLLILL-GLPDLYR-LWRSRPWFGPLCLRLSLYVGEGCTYATLLH 128

Db 66 GLRLHYVLSLALSALLLVMPMELYNFVMSHPVWFGDLGCRGYFVRELCAATVLS 125

Qy 129 MTALSVERYLAICRPLRARLVTRRRVALLAVALLSAGPFLFVVGVEQD 182

Db 126 VASLSAEKCLAVCQLRRRLRLLTRRLSLVVASLGLPALPWAIVMGQHE 179

RESULT 6

JC8012

C:Protein-coupled neuropeptide pyrokinin-2 receptor (CG8795) - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004

C:Accession: JC8012

R:Rosenkilde, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; DeLotto, R.

Biochem. Biophys. Res. Commun. 309, 485-494, 2003

A:Title: Molecular cloning, functional expression, and gene silencing of two *Drosophila*

A:Reference number: JC8011; PMID: 12951076

A:Accession: JC8012

A:Molecule type: mRNA

A:Residues: 1-595 <ROS>

A:Cross-references: GB:AV277899

C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as

e, feeding, and behavior.

C:Genetics:

A:Gene: CG8795

C:Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 12.8%; Score 261; DB 2; Length 595;

Best Local Similarity 29.7%; Pred. No. 2.3e-12;

Matches 78; Conservative 37; Mismatches 104; Indels 44; Gaps 8;

Qy 34 PLGLVPVTVAVCLCLFVVGSGNVVTMLIGRYDMRTTNLYLGMAVSDLLILL-CLP 92

Db 58 PLSLLATLUSGVALIFAGVLGNLTICIVISRNFMFTATNPFPLNLAISDMILLCSGMP 117

Qy 93 FDLVLRMRSPWFGPLCLRLSLYVGEGCTYATLHMTALSVERYLAICRPLRARLVTR 152

Db 118 QDLNLMHPDNPYPSDSICILESVLSEANATVLTITAFVVERVIAICHPRQHTMSKL 177

Qy 153 RVRRLIAVLAVALLSAGPFLFVVGVEQDPSGVVGLNGTARIASS-----PLASSPPL 208

Db 178 SRVAKFIAIWAALLALPQAQPSV-----VWQMGWGSCTCKMKNDFFAHFAVSGFL 230

Qy 209 WLSRAPPSPSGPTA-----EAAALFSREC-----RSPALGALRWML 249

Db 231 PF-----GGPMTAICVLYLVIGVKLRSLRLQALPRRCYDVNRGISAQTRVIRMLV 281

Qy 250 WVTYAYF--FLPFLC--LSILYG 268

Db 282 AVAVAFICWAPFHAQRLMAVYG 304

RESULT 7

TI5816

C:Keywords: hypothetical protein C48C5.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: TI5816

R:Pavello, A.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of *C. elegans* cosmid C48C5.

A:Reference number: Z18410

A:Accession: TI5816

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-378 <FAV>

A:Cross-references: UNIPROT:Q18701; EMBL:U39994; NID:g1055102; PID:g1055105; PIDN:AAB370

A:Experimental source: strain Bristol N2; clone C48C5

C:Genetics:

A:Gene: CESP:C48C5.1

A:Map position: X

A:Introns: 53/3; 87/2; 136/2; 169/3; 209/3; 231/3; 259/3; 286/1; 327/1

C:Superfamily: adenosine receptor A1

Query Match 12.5%; Score 255.5; DB 2; Length 378;

Best Local Similarity 27.0%; Pred. No. 3.9e-12;

Matches 66; Conservative 49; Mismatches 96; Indels 33; Gaps 6;

Qy 38 LVPVAVCLCLFVVGSGNVVTMLIGRYDMRTTNLYLGMAVSDLLILL-LGLPFDLY 96

Db 51 LYKVTALYIFLFGVIGNTTCLVMKPKPMKTHASWYLNLAIVSDLVTLVGLPFEVM 110

Qy 97 RLWRSRPWFGPLCLRLSLYVGEGCTYATLHMTALSVERYLAICRPL-RARVLVTRRV 155

Db 111 MNWQYWPFPDYICNLKALIAETTSVSIILTIFAIRYVAVCHPLFLMKVQPFKNI 170

Qy 156 RALLAVLMAVALLSAGPFLFVVGVEQDPSGVVPLNGTARIASSPLASSPPLMSRAP 215

Db 171 GTIIGTWIFSILCAMP--FAIHRADYIMKSWGTDNRIPVKSSKMCN----- 217

Qy 216 PSPSPGPETAFAAALFSRECRPSPAQLGALRWML-WVTYAYFFLPFLCLSLYLIGLREL 274

Db 218 -----IAYWF-----EPKLASTFKILFHSAIAFFALPLFTVILYARIACKV 260

Qy 275 WSSR'278

Db 261 SSNR 264

RESULT 8

JC2421

C:Protein-coupled receptor homolog, MOR-C - mouse

C:Species: *Mus musculus* (house mouse)

C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C:Accession: JC2421; I49122

R:Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi, T.

Biochem. Biophys. Res. Commun. 205, 1353-1357, 1994

A:Title: Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor

A:Reference number: JC2434; MUID:95100967; PMID:7802669

A:Accession: JC2421

A:Molecule type: mRNA

A:Residues: 1-367 <NTS>

A:Cross-references: UNIPROT:P35377; DBJ:D31663

R:Halford, W.P.; Gebhardt, B.M.; Carr, D.J.

J. Neuroimmunol. 59, 91-101, 1995

A:Title: Functional role and sequence analysis of a lymphocyte orphan opioid receptor.

A:Reference number: I49122; MUID:95318231; PMID:7797625

A:Accession: I49122

A:Status: preliminary; translated from GB/EMBL/DBJ


```
Db 44 PLGLKVTIVGLYLAVCIGLLGNCLVMYVILRHTKMTATNIYIFNLALADTLVLLTLPF 103
Qy 94 ---DLYRLWRSRPWVFGPFLCRLSLYVGEGETYATLLHMTALSVERYLAICRPLRARVLV 150
Db 104 QGTDILLGF----WFGNALCKTVIAIDYNNMFTSTFTLTAMSDVRYVAICHPIRALDVR 159
Qy 151 TRRRVRALIAVLWAVALLSAGPFLVGVGEQDPGIVVVGPLNGTARIASSPPLPWL 210
Db 160 TSSKAQAVNVAIWALASV-----VGVPVAINGSAQVDEBIEC-----L 198
Qy 211 SRAPPPSPSPETAEEAALFSRECRPSPAQLGALRVMLWVTAVFFLPFLCLSLYGLI 270
Db 199 VEIPAPQDYWGPFVAICIFLFS-----FIIPVLISVCYSIM 235
Qy 271 GRELWSSRRPLRGPAASGRGRHQTVRVLR 301
Db 236 IRLRGVR-----LLSGSREKDRNLRI 260

RESULT 11
S43087
orphan opioid receptor ORL1 - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S43087; G01892
R:Moillerieu, C.; Parmentier, M.; Mailleux, P.; Butour, J.L.; Moissand, C.; Chalon, P.; Ca
FEBS Lett. 341, 33-38, 1994
A:Title: ORL1, a novel member of the opioid receptor family. Cloning, functional expres
A:Reference number: S43087; MUID:94185768; PMID:8137918
A:Accession: S43087
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-370 <MOL>
A:Cross-references: UNIPROT:P41146; EMBL:X77130; NID:G471316; PIDN:CAA54386.1; PID:G4713
R:Lee P., H.
submitted to the EMBL Data Library, June 1995
A:Reference number: H00703
A:Accession: G01892
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-370 <LEE>
A:Cross-references: EMBL:U30185; NID:g1144296; PIDN:AAA84913.1; PID:g1144297
C:Genetics:
A:Gene: GDB:OPRL1
A:Cross-references: GDB:345029
A:Map position: 8q11.2-8q11.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.4%; Score 253.5; DB 2; Length 370;
Best Local Similarity 26.9%; Pred. No. 5.4e-12;
Matches 73; Conservative 46; Mismatches 95; Indels 57; Gaps 6;

Qy 34 PLGALPVTAVCLCLFVGVGVGNVVTVMIGRYDRMTTNNLYGSMVSDLLILLGLPFP 93
Db 47 PLGLKVTIVGLYLAVCIGLLGNCLVMYVILRHTKMTATNIYIFNLALADTLVLLTLPF 106
Qy 94 ---DLYRLWRSRPWVFGPFLCRLSLYVGEGETYATLLHMTALSVERYLAICRPLRARVLV 150
Db 107 QGTDILLGF----WFGNALCKTVIAIDYNNMFTSTFTLTAMSDVRYVAICHPIRALDVR 162
Qy 151 TRRRVRALIAVLWAVALLSAGPFLVGVGEQDPGIVVVGPLNGTARIASSPPLPWL 210
Db 163 TSSKAQAVNVAIWALASV-----VGVPVAINGSAQVDEBIEC-----L 201
Qy 211 SRAPPPSPSPETAEEAALFSRECRPSPAQLGALRVMLWVTAVFFLPFLCLSLYGLI 270
Db 202 VEIPTPDQYWGPFVAICIFLFS-----FIVPVLISVCYSIM 238
Qy 271 GRELWSSRRPLRGPAASGRGRHQTVRVLR 301
Db 239 IRLRGVR-----LLSGSREKDRNLRI 263
```

RESULT 12

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JC8011
G protein-coupled neurotrophin-2 receptor (CG8784) - fruit fly (Drosophila mel
C:Species: Drosophila melanogaster
C>Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C:Accession: JC8011
R:Rosenkild, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; DeLotto, R
Biochem. Biophys. Res. Commun. 309, 485-494, 2003
A:Title: Molecular cloning, functional expression, and gene silencing of two Drosophila
A:Reference number: JC8011; PMID: 12951076
A:Accession: JC8011
A:Molecule type: mRNA
A:Residues: 1-658 <ROS>
A:Cross-references: GB:AY277898
C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as
evolution, diapause, feeding, and behavior.
C:Genetics:
A:Gene: CG8784
A:Introns: 160/1; 215/2; 259/3; 326/1; 400/3
C:Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 12.4%; Score 252.5; DB 2; Length 658;
Best Local Similarity 30.8%; Pred. No. 1.1e-11;
Matches 92; Conservative 43; Mismatches 103; Indels 61; Gaps 14;

Qy 1 MGSPWNGSDGPEGAREPPWPALPPCDERRCSPFPLGALVPVTVAVCLC---LPVVGVSGNV 57
Db 83 LGST-NGTNASTMAAD-----SPVDE-----SLTETALTVCYALFVAGVGLN 126
Qy 58 VTVMIGRYDRMTTNNLYGSMVSDLLILL-GLPFDLYRLWRSRPWVFGPFLCRLSLY 116
Db 127 ITCVISRNNPMHTATNPFYFNLAVSOLLVSGIQELYNLWYPMYPTDAMCMGVS 186
Qy 117 VGECTVATLHMTALSVERYLAICRPLRARVLVTRRRVRLIAVLWAVALLSAGP--FL 174
Db 187 LSEMAANATVITITFTVRYIAICHPROHTMSKLSRAIKFIFAIWLAFLALPQAMQ 246
Qy 175 FLVGVGEQDPGIVVVGPLNGTARIASSPPLSPPPLWLSRAPPPSPGPETAEEAALF--- 231
Db 247 FSV-VYQNEGVSCTMENDFYAHV-----FVSGGFIFP-----GGPMTA-ICVLYVLI 291
Qy 232 -----SRECRPSP-----AQGLARVLMVWVTAYF--FLPFLC--LSLYGL 269
Db 292 GVKLRSLQLSPRTPTDANRGLNAQGRVIRMLVAVAFVFLCWAPPHQAQLMAVYGL 350

RESULT 13
157940
somatostatin receptor 5 - rat
N:Alternate names: somatotropin release-inhibiting factor subtype 28 receptor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: 157940; 157949; S39244
R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 42, 939-946, 1992
A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A:Reference number: 157940; MUID:93125499; PMID:1362243
A:Accession: 157940
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-363 <OCAL>
A:Cross-references: UNIPROT:P30938; GB:L04535; NID:G409238; PIDN:AAA17029.1; PID:G409239
R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 44, 1278, 1993
A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A:Reference number: 157949; MUID:94088493; PMID:8264565
A:Accession: 157949
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 341-363 <OCA2>
A:Cross-references: GB:S67370; NID:G455947; PIDN:AAB29371.1; PID:G455948
A:Experimental source: pituitary
```

R;Penetta, R.; Greenwood, M.; Patel, Y.C.
submitted to the EMBL Data Library, August 1993
A;Description: Correction of the nucleotide and amino acid sequence of the rat somatostatin
A;Reference number: S39244
A;Accession: S39244
A;Molecule type: mRNA
A;Residues: 309-363 <PEN>
A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
C;Genetics: SSTR5
C;Superfamily: vertebrate rhodopsin

Query Match 12.3%; Score 250.5; DB 2; Length 363;
Best Local Similarity 26.7%; Pred. No. 8.9e-12;
Matches 76; Conservative 43; Mismatches 99; Indels 67; Gaps 8;

QY 5 WNGSDPEGAREPPWALPCDERRCSPPLGA---LVPVAVCLCLFVGVSGNVVTVM 61
Db 12 WNASAASSGNHN--WSLVG-----SASPMGARAVLVPVLYLLVC--TVGLSGNTLVI 60
QY 62 LIGRYDRMRTTNLYLGSMVSDLLILGLPFDLYRLWSRPVFGPLLCRLSLYVGEGC 121
Db 61 VVLRHAKMTVNTVILNLAADVLEMLGLPFLATONAVVSWPFGSFLCLRLVMTLDGIN 120
QY 122 TVATLLHMTALSVRYLAICRPLARVLTTRRRVRLIALVLAVALLSAGPFLFLVGVQ 181
Db 121 QETSIFFCLMVMSVDYLVAVVPLRSARWRPRVAKWASAAVWVSLMSLPLLVFADVQ 180
QY 182 DPGISVVGNGTARTASSPLASSPLMTSRAPPPSPGPTAEAAALFSRECRPSPAQ 241
Db 181 G-----WGTGCLNS-----W-----PEPVG 194
QY 242 LGALRWLMVMTTAYFFLPFLCLSLYGLI-----GRELWSSRR 279
Db 195 LWGAAPITTSVLGPFGLLVLCCLVLLIVKAKAGRVGSSRR 239

RESULT 14

JC2459
Gastrin/cholecystokinin B receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: JC2459
R;Blandizzi, C.; Song, I.; Yamada, T.
Biochem. Biophys. Res. Commun. 202, 947-953, 1994
A;Title: Molecular cloning and structural analysis of the rabbit gastrin/CCKB receptor
A;Reference number: JC2459, MUID:94324990; PMID:8048969
A;Accession: JC2459
A;Molecule type: mRNA
A;Residues: 1-452 <BLA>
A;Cross-references: UNIPROT:P46627; GB:L31548; NID:g495663; PIDN:AAA31194.1; PID:g495665
C;Genetics:
A;Introns: 49/1; 133/1; 216/2; 273/1
C;Superfamily: neurokinin 1 receptor
C;Keywords: receptor; transmembrane protein
F;56-79/Domain: transmembrane #status predicted <TM1>
F;85-104/Domain: transmembrane #status predicted <TM2>
F;130-149/Domain: transmembrane #status predicted <TM3>
F;169-187/Domain: transmembrane #status predicted <TM4>
F;217-237/Domain: transmembrane #status predicted <TM5>
F;339-359/Domain: transmembrane #status predicted <TM6>
F;381-400/Domain: transmembrane #status predicted <TM7>

Query Match 12.2%; Score 249.5; DB 2; Length 452;
Best Local Similarity 25.2%; Pred. No. 1.3e-11;
Matches 86; Conservative 50; Mismatches 122; Indels 83; Gaps 10;

QY 48 LFVVGSGNVVTVMILIGRYDRMRTTNLYLGSMVSDLLILGLPFDLYRLWSRP--- 103
Db 62 IFLMSVGNVLIIVVLGSLRRLRTVNAFLSLAVSDLLAVACMPFTLL-----PNLM 115
QY 104 --WVFGPLLCRLSLYVGEGCTVATLLHMTALSVRYLAICRPLARVLTTRRRVRLIA 161

Db 116 GTTFFIGTICKAVSYLMGVSVSTLSLVAIALERYSAICRPLQARVWQTRSHAARVILA 175
QY 162 LWAVALLSAGPFLFVLGVQDPFGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPSG 221
Db 176 TWLLSGLLMVPPVYTAQV-----PVG 197
QY 222 PETAEAAALFSRECRPSPAQLGALRWLMVMTTAYFFLPFLCLSLYGLIGRELWSSRR-- 279
Db 198 FRLVLCQVHRW-----PSARVQQTWSVLLLL--LUFFFVGVMVAVAYGLISRELYLGLRFD 250
QY 280 -----PLRGPAAQRERGRHQTQVRLRWKWSRRGSK-DACLQSAAPPQTQT 323
Db 251 SDSSESQSRYRGQGLPGGAAPGV---HQNGRCRPEAGLAGEGDCGYQLPRSR--- 304
QY 324 LGPILPLAQLWAPIPAPPPISIPASTRRGGSGYINLLVAL 364
Db 305 --PALEALSALTAPISGPGPRPAQAKILAKRVVRMLLVI 343

RESULT 15

A46195
cholecystokinin B receptor subtype - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46195
R;Wank, S.A.; Pisegna, J.R.; de Weerth, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 8691-8695, 1992
A;Title: Brain and gastrointestinal cholecystokinin receptor family: structure and function
A;Reference number: A46195; MUID:92409582; PMID:1528881
A;Accession: A46195
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-452 <WAN>
A;Cross-references: UNIPROT:P30553; GB:M99418; NID:g203459; PIDN:AAA40925.1; PID:g203460
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:114083, NCBI:P114084)
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.2%; Score 249.5; DB 2; Length 452;
Best Local Similarity 26.1%; Pred. No. 1.3e-11;
Matches 84; Conservative 51; Mismatches 96; Indels 91; Gaps 13;

QY 48 LFVVGSGNVVTVMILIGRYDRMRTTNLYLGSMVSDLLILGLPFDLYRLWSRP--- 103
Db 64 IFLMSVGNVLIIVVLGSLRRLRTVNAFLSLAVSDLLAVACMPFTLL-----PNLM 117
QY 104 --WVFGPLLCR-LSLYVGEGCTVATLLHMTALSVRYLAICRPLARVLTTRRRVRLIA 160
Db 118 GTTFFIGTICKAVSYLMGVSVST-LNLVAIALERYSAICRPLQARVWQTRSHAARVIL 176
QY 161 VLWAVALLSAGPFLFVLGVQDPFGISVVPGLNGTARIASSPLASSPPLWLSRAPPPSPS 220
Db 177 ATWLLSGLLMVPI-----PVYTMV-----QP 198
QY 221 GPETAEAAALFSRECRPSPAQLGALRWLMVMTTAYFFLPFLCLSLYGLIGRELW----- 275
Db 199 GPRVLCQVHRW-----PSARVQQTWSVLLLL--LFFIFGVVIAVAYGLISRELYLGLHF 251
QY 276 -----SSRRPLRGPAAAG---RERGRHQTQVRLRWKWSRRGSKDACLQSAAPPQT 320
Db 252 DGENSETQSRARNQGGPLGGAAPGVHQNGGCRPVTSVAGE-----DSDGCCVQLPRSR 306
QY 321 AQTGLPLLAQLWAPLPAPP 342
Db 307 LE-----MTLITFTPGGVP 321

Search completed: April 11, 2005, 21:05:37
Job time : 18.4461 secs